GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

November 13, 2005, 08:31:17; Search time 84 Seconds (without alignments) 1944.682 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-606-300-11 1619 1 WTKIELRALGNYGLKVSAVG......VEAILEPVKNLTWPSGIHQN 319

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

UniProt\_03:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	ಹ			Q6bdj2 spinacia ol			Q9vgf3 drosophila			Q20127 caenorhabdi		O9vgf2 drosophila		Q6fu59 candida gla					Q6cig5 kluyveromyc				Q89vc3 bradyrhizob		Q65hs3 bacillus li	Q8ua47 agrobacteri	Q7xej9 oryza sativ	Q6bpt1 debaryomyce		8	Q8etf4 oceanobacil
SUMMAKIES		ព		Q84LI1	Q84L20	Q6BDJ2	Q8A1P5	Q7UZ40	Q9VGF3	Q7QHC3	Q9VGF1	020127	Q8PF04	Q9VGF2	Q8P3K6	Q6FU59	QGBZUS	Q75DD3	Q82N99	Q7S6W9	Q6CIG5	Q826A9	Q52472	Q9KE47	Q89VC3	YMT1 YEAST	Q65HS3	Q8UA47	Q7XEJ9	Q6BPT1	Q9RJW1	Q7NMC8	Q8ETF4
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	Query	Match	100.0	83.3	81.7	77.9	42.9	38.6	36.7	•	33.6	31.1	26.3	26.0	25.8	25.6	25.5	23.9	23.7	23.3	23.2	22.8	22.6	22.4	22.3	22.1	21.6	21.4	21.4	21.3	21.3	21.2	21.2
		Score	1619	1348	1322	1261	695	625	593.5	593	544.5	503	426	420.5	417.5	414.5	413	387.5	383	378	375	369.5	366	362.5	361	358	349	346.5	346.5	345		4	342.5
	Result	No.	-	~	m	4	S	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

SEQUENCE REAM N.A.
MEDLINE=22043773; PubMed=12047629;
MEDLINE=22043773; PubMed=12047629;
Gatzek S., Wheeler G.L., Smirnoff N.;
"Antisense suppression of 1-galactose dehydrogenase in Arabidopsis thaliana provides evidence for its role in ascorbate synthesis and reveals light modulated 1-galactose synthesis.";
Plant J. 30:541-553(2002).

REFERENCE

Ecker J.R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

		Q6he69 bacillus th Q6f7z6 acinetobact	-	Q/31K1 pacilius ce Q635i5 bacillus ce	Q92td8 rhizobium m	Q8uad6 agrobacteri	-	Q8g5a3 bifidobacte
2818Z0 YQKF_BACSU	7NK63 81MD1	26HE69 26F7Z6	6DAK3	Q731K1 Q6351S	92TD8	SBUADE	BFGXS	28G5A3
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339	336.5 329.5	329.5	327	325.5 323.5	323.5	317	315	314
33	34 35	36 37	38	40	41	4.4	44	45

## ALIGNMENTS

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01-JUN-2003
01-JUN-2003
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Galactose dehydrogenase.
Actinidia deliciosa (Kiwi).
Bukaryoct; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
Bricales; Actinidiaceae; Actinidia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTKIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYG
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                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO31394; CAA2680.1; -.
EMBL; AVC50377; AAK91395.1; -.
EMBL; AVC90337; AAL90998.1; -.
EMBL; AL1563; CAD10386.1; -.
EMBL; AL161583; CAB80084.1; -.
EMBL; AL161583; CAB800888; Aldo, ket_red; I.
EMINTS; PRODOMS PRODORS8; Aldo, ket_red; I.
              SEQUENCE FROM N.A.
Obermaier B., Deutschenbaur S., Piravandi E., Mewes H.W.,
Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beuning L., Bowen J., Crowhurst R., Gleave A., MacRae E., Perera S., Ross G., Snowden K., Walton E., Yauk Y.K.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                     Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 319 AA; 34531 MW; 9400717380DFA71E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 1619; DB 2;
100.0%; Pred. No. 1.5e-107;
ive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 319; Conservative
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SEQUENCE FROM N.A.
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Malus domestica (Apple) (Malus sylvestris).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
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TISSUB-Pre-opened floral bud;
Beuning L., Bowen J., Crowhurst R., Gleave A., Macrae E., Newcomb Perera S., Ross G., Snowden K., Walton E., Yauk Y.K.;
Submitted (MAY-2003) to the EWBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                         Length 319;
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TISSUB-Pre-opened floral bud;
Laing W.A., Macrae E.;
Submitted (MAK-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AYZ64803; AAP21783.1; -.
HISSP; OYA237; 1JBZ.
InterPro; 1PR001395; Aldo/ket red.
Pfam; PF00248; Aldo/ket red; T.
ProDom; PR00069; ALDKGFRDTASAS.
ProDom; PD000288; Aldo/ket red; 1.
SEQUENCE 324 AA; 34974 WW; OBFB0C8A18A04169 CRC64;
TISSUE-Developing shoot buds;
Laing W.A., MacRae E.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AXIJ6585; AA016639.1; -.
InterPro; IPR001395; Aldo/ket_red.
PRINTS; PR00069; ALDKETFRTASE.
PRINTS; PR00069; ALDKETFRTASE.
PRODOM; PD000288; Aldo/ket_red; 1.
SEQUENCE 319 AA, 34539 MW; 8657434C03520FAB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                   83.3%; Score 1348; DB 2;
80.5%; Pred. No. 3.4e-88;
ive 32; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.7%; Score 1322; DB 2; 77.7%; Pred. No. 2.5e-86;
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                                                                                                                                                                                                                                                                                               Best Local Similarity 80.5%
Matches 256; Conservative
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Best Local Similarity
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NCBI TaxID=3750;
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246 CKXNGKNISKTALQYSLSNKDISTTLVGMNSVKQVEENVGAALELETAGKDEKTFAEIEN 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 ILHCHDIBFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVDVI 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 VAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGMDQETLSE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=VDI-5482 / ATCC 29148;
STRAIN=VDI-5482 / ATCC 29148;
STRAIN=VDI-5482 / ATCC 29148;
STRAIN=VDI-5482 / ATCC 29148;
MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299:2074-2076(2003).
Science 299:2074-2076(2003).
InterPro; IPR010395; Adfo/ket_red.
PEAM; PR00248; Addo/ket_red.
PEAM; PR00269; ALDKETRDTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 SEKWILGKGLKALQVPRSDYIVATKCGRY-KEG---FDFSAERVRKSIDESLERLQLDYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 IBLRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 LSYCHYGVNDSTILLDLIPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAA
             CKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVBENVAAVTELESLGMDQETLSEVEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
42.9%; Score 695; DB 2; Length 310;
Best Local Similarity 43.1%; Pred. No. 1.5e-41;
Matches 135; Conservative 73; Mismatches 95; Indels 10;
                                                                                                                                                                                                                                                            Bacteroides thetaiotaomicron.
Bacteria Bacteroides (class); Bacteroidales;
Bacteroidaceae; Bacteroides.
NCBI_TaxID=818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 AA; 34831 MW; 2D6C1B689C1C5298 CRC64;
                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Q7UZ40

ID Q7UZ40

Q7UZ40;
AC Q7UZ40;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
                                                                                                                                                                       PRT;
                                                                    303 ILEPVIOLITWPSGING 318
                                                                                     300 VEAILEPVKNLTW 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VREIIGEOORVSW 307
                                                                                                                                                                                                                                                           OrderedLocusNames=BT3614;
                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                          Putative oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complete proteome SEQUENCE 310 AA
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              243
                                                                                                                                                                                   Q8A1P5;
                                                                                                                                           RESULT 5
Q8A1P5
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                                                                                   120
                                                                                                 LHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVDVIL 180
                                                                                                                                                        SYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAAV 240
                                                                                                                                                                                                                   SYCHYGINDSTLEDLIPYLKSKGVG1ISASPLAMGLLTENGPPEWHPASAELKSACRAAA 245
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                                                                                                                                                                                                                                                                          246 VYCKERGNNISKLALQYSLSNKOISSVLVGMNSINQVEENVAAAVELATIGKNEKILAEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MTKI ELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYG
                                                                                   GTLSEKMLGKGLKALQVPRSDYIVATKCGRYKEGFDFSAERVRKSIDESLERLQLDYVDI
                                                                                                                                                                                                                                                         241 AHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGMDQETLSEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mieda T., Yabuta Y., Rapolu M., Motoki T., Ishikawa T., Yoshimura K., Shigoka S., Tabuta Y., Rapolu M., Motoki T., Ishikawa T., Yoshimura K., Shigoka S., "Direct Submission.";
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, ABIGO90; BAD13687.1; -
InterPro; IPR001395; Aldo/ket_red; -
Pfam; PF00248; Aldo_ket_red; -
PRINTS; PR00069; ALGKETRDTASE.
PRINTS; PR00069; ALGKETRDTASE.
SEQUENCE 322 AA; 35262 WW; CB5BA18D81AZ7AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAAVAH
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 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spinacia oleracea (Spinach).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Baparatophyta; Magnoliophyta; eudicotyledons, core eudicots, Caryophyllales, Amaranthaceae, Spinacia.
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31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                    EAILEPVKNLTWPSGIHQN 319
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EAILKPVKNQTWPSGLQQS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L-galactose dehydrogenase.
Name=GDH;
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248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                 06BDJ2;
25-OCT-2004
25-OCT-2004
25-OCT-2004
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63

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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 IEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVDVILSYCHY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 RGSDIAXIALQFSIANEDFATCIPGSANPNRVAQWVEWAQE----PIDETLYAEVKEILK 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 RALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 MLGKGLKALQVPRSDYIVATKCGRYK-EGFDFSAERVRKSIDESLERLQLDYVDILHCHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAAVAHCKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGKKITKLALOYSLANKE1SSVLVGMSSVSQVEENVAAVTELESLGMDQETLSEVEA1LE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                             "Complete genome sequence of the marine planctomycete Pirellula {\tt sp.} strain 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                             MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pna8.1431443100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterayera, Endopterygota, Diptera, Brachycera, Muscomorpha, Psphydroidaa, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
                                                                                                Bacteria, Planctomycetes, Planctomycetacia, Planctomycetales, Planctomycetaceae, Pirellula.
                                                                                                                                                                                                                                                 Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
Schlesner H., Amann R., Reinhardt R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.6%; Score 625; DB 2; Length 347; 39.2%; Pred. No. 1.8e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.2%; Pred. No. 1.05-55, tive 78; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 AA; 39075 MW; 4721A31577F8702C CRC64;
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Putative oxidoreductase-possibly Aldo/keto reductase.
OrderedicousNames-RB203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                EMBL, BX294133; CAD71446.1; -
EMBL, BX294133; CAD71446.1; -
InterPro; IPR001395; Aldo,ket_red.
Prof0246; Aldo ket_red; I.
ProDom; PD000288; Aldo/Ket_red; I.
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Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                 Rhodopirellula baltica
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                                                                                                                                              NCBI_TaxID=117;
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School R. A., Nerdis S. E., Richards S. A., Change M. C., Feltic S. D., Mann K. H., Doyle C., Baxcer E. G., Hell G., Nelson C. R., Gabor G. L., Barchon R. C., Change M. C
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                                                                                                                                                                                                                                                                                                           257 KASEVCKERGVELGKLAMYYTMSGLPEVSTFLTGMQTRQLLRINLDA-NEVGLSDKEQEV 315
                                                                                                                                                                                                                                                               DILHCHDIEFG-SLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVD 177
                                                                                                                                                                                                                  21 RMEYRNIGKTGLQVSKVSFGGGALCANYGFDLE-EGIKTVHEAVKSGINYIDTAPWYGGG 79
                                                                                                                                                                                                                                                                                                                                            178 VILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTBQGPPEWHPASPELKSASK
                                                                                                                                                                                                                                                                                                                                                         197 TVLTYARYTLTDETLLEYLDFFKSQNLGVICAAAHALGLLTNAGPQPWHPASDEQXAIAR
                                                                                                                                                                                                      3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                   LSEKMLGKGLKALQVPRSDYIVATKCGRYK----EGFDFSAERVRKSIDESLERLQLDYV
                                                                                                                                                                                                                                                                                                                                                                                         AAVAHCKSKGKKI TKLALQYSLAN-KEISSVLVGMSSVSQVEENVAAVTELESLGMDQET
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukāryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!-CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
EMBL, AAABO1008816; EAA05276.1; -.
HSSP, PS2895; 1J05.
InterPro; IPR01395; Aldo/ket_red.
Pfam, PP00448; Aldo ket_red; 1.
PRINTS, PR00069; ALDKETRDTASE.
                                                                                                                                                                              11,
                                                                                                                                                         DB 2; Length 345;
                                                                                                                                                                               Indels
                                     Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases EMBL; AB003694; AAF54729.1; -. HSSP; P52895; 1J96. PlyBase; FBgn0037973; CG18547.
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                     InterPro; IPR001395; Aldo/ket_red.
Pfam; PR00248; Aldo ket_red; 1.
PRINTS; PR00069; ALDKTRTDTASA.
PRODOM; PD000289; ALDKTRTPASA.
SEQUENCE 345 AA; 38868 WW; 86124CBB34BF04F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38590 MW; 52B38ADD54170598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
EbiP8370 (Fragment).
                                                                                                                                                       Query Match 36.7%; Score 593.5; DB 2; Best Local Similarity 42.5%; Pred. No. 3.1e-34; Matches 128; Conservative 63; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=ebiG8370; ORFNames=ENSANGG0000006316;
Anopheles gambiae str. PEST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    L 297
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MEDINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Addman M.D., Celniker S.E., Holt R.A., Evana C.A., Galle R.E., Admanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.E., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Stutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Chang Q., Chen L.X.,

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RA Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,

Rabeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boldshakov S.,

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Rabeson K.Y., Benos P.V., Bernos B.P., Bhandari D., Boldshakov S.,

Raberis K.C., Bussam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Raberis K.C., Bussam D.A., Butler H., Cadieu E., Center R.,

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Raberis K.C., Busnam D.A., Butler H., Cadieu E., Conter S.,

Raberis K.C., Busnam D.A., Butler H., Cadieu E., Candres S.,

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Raberis R. McIntosh W. Mobarry C., McLeod D. W. Wobarry C., McLeod D. W. Nobarry C., McLeod D. W., Nobarry
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                                                                                                                                                                          3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
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Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bhydroidea; Drosophilidae; Drosophila.
        Length 342;
Query Match 36.6%; Score 593; DB 2; Length 34 Best Local Similarity 39.7%; Pred. No. 3.4e-34; Matches 126; Conservative 68; Mismatches 105; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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MEDLINE=22426069; PubMed=12537572;

Mistas S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

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Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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EMBL; AE003694; AAFS4731.1; -.
EMBL; AX118797; AAMS0657.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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InterPro; IPR001395; Aldo/Ket red.
Pfam; PF00248; Aldo ket red.
PRINTS; PR00069; ALDKETRDFASE.
SEQUENCE 342 AA: 1900.
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SEQUENCE FROM N.A.
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Celniker S.;
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62 TLSEKMIGKGLKALQVPRSDYIVATKCGRYK----EGFDFSAERVRKSIDESLERLQLDY 117
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                                                                Gaps
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
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   Length 342;
                                                          Indels
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"The sequence of C. elegans cosmid F37C12.";
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
33.6%; Score 544.5; DB 2; 36.6%; Pred. No. 9.8e-31; ive 71; Mismatches 117;
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01-NOV-1996 (TrEMBLrel. 01, Last
01-OCT-2003 (TrEMBLrel. 25, Last
Hypothetical protein F37C12.12.
ORFWames=F37C12.12;
                                                                Matches 117; Conservative
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 5. Part 101;

MEDLINE=22022145; Pubmbd=12024217; DOI=10.1038/417459a;

A SILva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

A Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

A Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

Camarcotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

A Raia J.B., Ferreira A.J.S., Ferreira A.C., Ferro M.I.T.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

A Ratsuyama A.M., Machado M.A., Maddeira A.M.B.N., Martinez-Rossi N.M.,

Martins B.C., Machado M.A., Maddeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

Trindade dos Santos M., Tuffil D., Tsai S.M., White F.F.,

Stubal J.C., Kitajima J.P.;
                                                                                                                                                                                                                                                                                            63 LSEKMLGKGLKALQVPRSDYIVATKCGR----YKEGFDFSAERVRKSIDESLERLQLDYV 118
                                                                                                                                                                                                                                                                                                                                                                                          DI--LHCHDIEFGSLDQIV-SETIPALQKLKQEGKTRFIGITGLPLD----IFTYVLDRV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 PPGTVDVILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPE 231
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                                                                                                                                                                                              3 KIELRALGNIGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT 62
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                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                42;
                                                                                                Length 439;
                                                                                           31.1%; Score 503; DB 2; Length 43 36.8%; Pred. No. 1.2e-27; ive 58; Mismatches 106; Indels
                         Hypothetical protein.
SEQUENCE 439 AA; 49696 MW; B0508EB84720FFCD CRC64;
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Last annotation update)
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PD000288; Aldo/ket_red; 1.
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ProDom; PD000288; Aldo/Ket_red; 1.
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EMBL; AE012069; AAM39019.1; -.
HSSP; P52895; 1J96.
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                                                                                        Query Match
Best Local Similarity 36.8
Matches 120; Conservative
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01-OCT-2002
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  ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SASPLAMGLITE-QGPPEWHPASP----BLKSASKAAVAHCKSKGKKITKLALQYSLANK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Addms M. D., Celniker S. E., Holt R. M., Evans C.A., Gocayne J.D., Addms M. D., Celniker S. E., Holt R. M., Evans C.A., Gocayne J.D., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortenan J. R., Yandell M.D., Zhang Q., Chen L. X., Anton G.G., Wortenan J. R., Yandell M.D., Zhang Q., Chen L. X., Abrid G., Wortenan J. R., Yandell M.D., Zhang Q., Chen L. X., Gabor G.L., Abril J. F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Abril J. F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxeer B.G., Helt G., Nelson C. R., Gabor G.L., Abril J. F., Agbayani A., Berson K.Y., Benos P.V., Berman B. P., Bhandari D., Bolshakov S., Ballew R.M., Baul D., Botchan M.R., Buller H., Caddeu B., Center A., Chandra I., Borkova D., Botchan M.R., Buller H., Caddeu B., Center A., Chandra I., Antist R.C., Busam D.A., Buller H., Caddeu B., Center A., Chandra I., Antist R. C., Berngelista C.C., Ferraz C., Ferriera S., Fleischmann W., A Dourbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Goos P., Goorell J. Heiman T.J., Hernandez J.R., Houck J., Alastin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Alastin D., Houston K.A., Howland T.J., Hernandez J.R., Kolly D., Lai Z., Alastin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., Alasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattel B., McIntosh T.C., McLeod M.P., Morbherson D., Merkuloy G., Milshina N.V., Mobarry C., Morris J., Morbherson D.,
                                                                                                                                                                                                                                                                                                                                                                         101
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                                                                                                                                                                                                                                                             GTLSEKMLGKGLKALQVPRSDYIVATKCGRY-----KEG-----FDFSAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRKSIDESLERLQLDYVDILHCHDI------EFGSLDQIVSETIPALQKLKQEGKTRF
                                                                                                                                                                                                                           1 MTKIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYG
                                                                                                                                                  Gapa
                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263 EISSVLVGMSSVSQVBENVAAVTELESLGMDQETLSEVEAILEPVKNLTW 312
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Bukaryota; Metazoa; Arthropoda; Haxapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                     Query Match 26.3%; Score 426; DB 2; Length 336; Best Local Similarity 33.7%; Pred. No. 2.8e-22; Matches 118; Conservative 60; Mismatches 104; Indels
34982 MW; 8BF6EA56C8E68E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
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ORFNames=CG12224;
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Sanders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
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A Williams R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Mang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodager, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhang L.,
Zheng X.H., Zhong F.N., Zhang W., Zhau S., Zhu S., Smith H.O.,
Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                             MEDLINE=22426065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodson A., George R.A., Hoskins R.A., Lestiffer B.D., Richards S., Sodergren E.J., Pacileb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Frinshing a Whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Taminker J.S., Hoteler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celni, Wesler D.B.,
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDILINE-22426069; PubMed=12537572;

Mista S., Crosby M.A., Mangall C.J., Matthews B.B., Campbell K.S.,

Mista S., Crosby M.A., Mannall C.J., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,

Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harxis N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.0%; Score 420.5; DB 2; Length 3 Best Local Similarity 33.7%; Pred. No. 5.9e-22; Matches 102; Conservative 57; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Subjected (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003694; AAFS4730.1; --
FlyBase; FBgn0037974; CG12224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 AA; 32984 MW; 8B03E0F0C8EE1B8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomics perspective.",
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CSTRAIN=ATCC 33913 / NCPPB 528;

CM REDIANE=22022145; Pubmed=12024217; DOI=10.1038/417459a;

CM SIIVA A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

CM SIIVA A.C.R., Ferro J.A., Vanisham A.A., Almeida N.F.,

CM Andes L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

CAMARCOTE G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

CICATELLI R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

CICATELLI R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Ratia J.B., Ferranco M.C., Greggio C.C., Gruber A.,

Ratsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Coali E.C., Machado M.A., Maddeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Maddeira A.M.B.N., Martinez-Rossi N.M.,

Moreliza L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Takita M.A., Taudia B.C., Teata R.I.D.,

Trindade dos Santos M., Truffilm J. Trail S.M., White F.F.,

Setubal J.C., Kitajima J.P.;
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                                                         DILHCHDIBEG-SLDQIVSBTIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVD
                                                                                          178 VILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASK
                                                                                                                                                                                                                                                                                             238 AAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGM---DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 LGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEKML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xanthomonas campestris (pv. campestris).
Bacteria, Proteobacteria, Gammaproteobacteria, Xanthomonadales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 AA; 34773 MW; 36B212C16AFA2F1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25.8%; Score 417.5; DB 2 35.2%; Pred. No. 1.1e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 417:459-463(2002).
EMBL, AE012528; AAM43286.1; -.
Interpro, IPR001395; Aldo/ket_red.
Pfam; PF00248; Aldo ket red; I.
ProDom; PD000288; Aldo/ket_red; I.
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OrderedLocusNames=XCC4065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                               295 ETL 297
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247 AAEYTHKHGVEIQDLANRYAMFNWHKYGPTVIGVSNVAELQDAIIDYQITEKDKL--PEN 304
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Gafard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne B., Bleykasten C.,
B Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Royer J., Cattolico L., Confanioleri F., de Daruvar A.,
Boisrame A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G., Straub M.L., Suleau A.,
Swennene D., Tekaia P., Wesolowski-Louvel M., Westhof E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
M. Genome evolution in yeasts.";
                                  181 SYCHYGVNDSTLLDLLPYL-KSKGVGVIS-ASPLAMGLLTEQGPPEWHPASPELKSASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GSVFGPVAEDD----AVATVREAFRLGINFFDTSPYYGGTLSEKMLGKGLKALQV--PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 SDYIVATKCGRYKEG-FDFSAERVRKSIDESLERLOLDYVDILHCHDIBFGSLDQIVSET
                                                                                                      239 AVAHCKSKGKKITKLALQYSLAN-KEISSVLVGMSSVSQVEENVA--AVTELESLGMDQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORFNames=YALIOF30811g;
Yarrowia lipolytica CLIB99.
Succharomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|Q04212 Saccharomyces cerevisiae YMR041c unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.5%; Score 413; DB 2; Length 330; 36.0%; Pred. No. 2.3e-21; rative 57; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001395; Aldo/ket_red.
Pfam; PF00248; Aldo ket_red; I.
PRINTS; PR00069; ALDXETRDTABS.
PPCDOm; P0000288; Aldo/ket_red; 1.
SEQUENCE 330 Aa; 36474 WW; 345DCDA8E7332A0D CRC64;
                                                                                                                                                                                                                                         305 DIKLVKHIQEEILGTEHYNETWDSGI 330
                                                                                                                                                                                                     TLSEVEAILEPV----KNLTWPSGI 316
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SEQUENCE FROM N.A.
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Q6BZUS;
                                                                                                                                                                                                                                                                                                                                   RESULT 15
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Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Goffard N., Frangeul L., Ahgle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Blaykasten C.,
Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyer P., Kachouri R.,
Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
Mincker P., Souciet J.L.;
T. "Genome evolution in yeasts.";
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                                                                                                                                                                                                       LLTE-QGPP---EWHPASPELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGM 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVSAVGFGASPLGSVFGPVAED-DAVATVREAFRLGINFFDTSPYYGGTLSEKMLGKGLK 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIFTYVLDRVPPGTVDVILSYCHYGVNDSTLLD-----LLPYLKSKGVGVISASPLAMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp[004212 Saccharomyces cerevisiae YMR041c.
ORFNames=CAGLOF06061g;
Candida glabrata CBS138.
Bukaryota; Pungi, Accomycota; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
[11]
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EMBL, CR380952; CAG59159.1; -.

InterPro; IPR001395, Aldo/ket red.

Pfam, PF00248; Aldo ket red.

PRINTS; RR00069; ALDKETRUTASE.

ProDom, PD000288; Aldo/ket red; 1.

SEQUENCE 336 AA; 38209 WW; 48EEBE66D6FE662F CRC64;
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Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                     298 RSVAEVQ 304
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Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J.,
Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
05-UTL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein Ti611.160 (Artq33670/Ti611 160) (L-galactose dehydrogenase) (Hypothetical protein Artq33670)
Name=Ti611.160; Synonyme=Artq33670, L-GalDH;
Arabidopsis thaliana (Mouse-ear cress).
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-UNITS=bits - START=1 - END=-1 - MATRIX=blosum62 - TRANS=human40.cdi - LIST=45
-DOCALIGN=200 - THR_SCORE=pct - THR_MAX=100 - THR_MIN=0 - ALIGN=15 - MODE=LOCAL
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-DSV TIMEOUT=120 - WARN TIMEOUT=30 - THRRADS=1 - XGAPEXT=0 - LONGLOG
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Q84120 malus domes
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Q8a1p5 bacteroides
Q7uz40 rhodopirell
Q9vgf3 drosophila
Q20127 caenorhabdi
Q8pf4 xanthomonas
Q9vff2 drosophila
Q9vff2 drosophila
Q8pf8 xanthomonas
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Q6bu5 yarrowia li
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(c) 1993 - 2005 Compugen Ltd.

    protein search, using frame_plus_n2p model

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                                                                            MEDLINE=22043773; PubMed=12047629; Gatzek S., Wheeler G.L., Smirnoff N.; Gatzek S., Wheeler G.L., Smirnoff N.; Ahtisense suppression of 1-galactose dehydrogenase in Arabidopsis thaliana provides evidence for its role in ascorbate synthesis and reveals light modulated 1-galactose synthesis."; Plant J. 30:541-553(2002).
           Saton
 Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL031394; CAA205801; -.
EMBL; AV090337; AAL909981; -.
EMBL; AV17563; CAD10386.1; -.
EMBL; AJ417563; CAD10386.1; -.
EMBL; AJ417563; CAB80084.1; -.
EMBL; AJ417699; TO4984.
                                          Ecker J.R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
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PRINTS; PR00069; ALDKETRDTASE.
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Actinidia deliciosa (Kiwi).
Bukaryota, Viridisplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
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Beuning L., Bowen J., Crowhurst R., Gleave A., MacRae E Perera S., Ross G., Snowden K., Walton E., Yauk Y.K.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
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SEQUENCE FROM N.A.

TISSUE=Developing shoot buds;

Laing W.A., MacRee E.;

Submitted (NOV-2002) to the EMBL/GenBank/DDBJ dat.

DR EMBL; AY176585; AA018639.1; -.

DR Pfam; PF00248; Aldo/ket red;

Probom; PRO0069; ALDKETROFASE.

Probom; PD000288; Aldo/ket red; 1.
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Mismatches:
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Q84L20;
01-UTM-2003 (TrEMBLrel. 24, Created)
01-UTM-2003 (TrEMBLrel. 24, Last sequence update)
01-UTM-2003 (TrEMBLrel. 26, Last annotation update)
1-galactose dehydrogenase.
Malus domestica (Apple) (Malus sylvestris).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
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TISSUB=Pre-opened floral bud;
TISSUB=Pre-opened floral bud;
Beuning L., Bowen J., Crowhurst R., Gleave A., Macrae E.
Perera S., Ross G., Snowden K., Walton E., Yauk Y.K.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
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TISSUB-Pre-opened floral bud;
TISSUB-Pre-opened floral bud;
TISSUB-Pre-opened floral bud;
TISSUB-Pre-opened floral bud;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ datab
EMBL; AY264803; AAP21783.1; -.
HASSP; O74237; JUEZ.
HINGSP; O74237; JUEZ.
PRODOS, PRO01395; Aldo/ket red;
PRODOM; PRO00269; ALDOKETPASE.
PRODOM; PRODOMS ALDOKETPASE.
SEQUENCE 324 AA; 34974 MW; OBFBOCBAIBAO4169 CRC
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Matches:
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                                 CGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCCCCCGTATTATGGAGGAACA
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01-Mar-2004 (TrEMBLrel. 26, Last anno
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Spinacia oleracea (Spinach).
Spinacia oleracea (Spinach).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Spinacia.
NCBI_TaxID=3562;
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Shigeoka S.;
Injecka S.;
Injecka S.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB160990; BAD32687.1; -
InterPro; IPR001395; Aldo/ket_red.
Fam; PP00248; Aldo ket_red; I.
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MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
Chiang H.C., Hooper L.V., Gordon J.I.;
"A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
Science 299.2074-2076(2003).
EMBL; AE016941; AA078119:1;
InterPro; IPR001395; Aldo/Ket_red.
Pfam; PF00248; Aldo ket_red; I.
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SerAsnProLys1leAlaThrThrLeuPheSerThrThrAsnProGluAsnValLysLys
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                                                               GCAAACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAGAA
                                                                                                                                               gb.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Pirellula.
NCBI_TaxID=117;
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EMBL: BX29413; ChD71446.1; --

InterPro; 1PR001395; Aldo/ket_red.

Pfam: PF00248; Aldo ket_red; I.

ProDom; PD000288; Aldo/ket_red; I.
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                                                                                                                                                                                                                                                                                                    AAGGCCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAGATTTCG
                                       ATTGACGAGAGCTTGGAGAGCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGAC
                                                                                                                    376 ATTGAGTTCGGGTCTCTTGATCAGATTGTGAGAACAATTCCTGCTGCTCTTCAGAAACTG
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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A Cherry J.W., Cawley S., Dallker C., Davengort L.B., Davies P.,

Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S. M.,

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MEDLINE-22426069; Pubmed=12537572;

Misra S., Croeby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

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Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Center A.,
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Busam D.A., Butler H., Cadieu E.,
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MEDLINE=22426070; Pubmed=12537573;
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01-MAR.2004 (TrEMBLrel. 26, Last sequence update)
01-MAR.2004 (TrEMBLrel. 26, Last sequence update)
01-MAR.2004 (TrEMBLrel. 26, Last annotation update)
01-MAR.2004 (Tremment).
Name=ebiG8370; ORFNames=ENSANGG0000006316;
Anophales gamblae str. PEST.
Anophales gamblae str. PEST.
Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TAXID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                       7.8
                                                                                                                                                                                                                                                                                                                                                                        Anopheles Genome Sequencing Consortium;
Submitteed (MAR-2002) to the BMBL/Genbank/DDBJ databases.
-|- CAUTION: The sequence shown here is derived from an
EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which
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HSSP; P52895; 1J96.
InterPro; IPR001395; Aldo/ket_red.
Pfam; PP00248; Aldo_ket_red; I.
PRINTS; PR00169; ALDKETRDTASE.
ProDom; PD000288; Aldo/ket_red; 1.
NON TER 1342 342
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SEQUENCE FROM N.A.
STRAIN=PEST;
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ThrMetSerGlyLeuProGluValSerThrPheLeuThrGlyMetGlnThrArgGlnLeu
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| AlaTyrProIleSerValLeuLysGluPheLeuThrArgThr---AlaGlyArgLeuAsp
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
InterPro, IPR001395; Aldo/ket_red.

Pfam; PF00248; Aldo ket_red; I.

PRINTS; PR00069; ALDKETEDTASE.

PRODOM; PD000288; Aldo/ket_red; 1.

SEQUENCE 345 AA; 38868 My; 86124CBB34BF04F2.
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63.46%
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Best Local Similarity:
Query Match:
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MEDLINE=20196066; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hookins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazel R.G., Champe M., Pfeiffer B.D., Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L., Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Benson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P., Auris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
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                                 ACAATTCCTGCTCTTCAGAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACT
                                                                            GGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGAT
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|SerGluLysGluAlaAspValLeuSerTyrLeuLysGluArgValPhePro 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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Gln11eAsnLeuAspAlaTyrPhe------
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Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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Science 287:2185-2195(2000).
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MEDLINE=22445065; PubMed=12537568;
MEDLINE=22445065; PubMed=12537568;
MEDLINE=22445065; PubMed=12. D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patk S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Man K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Free E., Wheeler D.A., Lewis S.B., Rubin G.M., Ashburner M., Celniker S.B.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-2242669; Pubmed=12537572; Matthews B.B., Campbell K.S., Misra B., Crosby M.A., Mungall C.J., Malthews B.B., Campbell K.S., Misra B., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Dryadale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Stapleton M., Brostein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases

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STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                       NCBI_TaxID=6239;
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SEQUENCE 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                                                                                                                                                                                                                                                                                                              Fulton L.;
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ThrAlaAlaLysAlaArgGluSerValLysArgSerLeuGluLeuGlnLeuAspArg 138
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ThralaTyrAspValAspValLeuLysGluCysAlaGluArg---GlyLysGlyArg1le 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCTGCAAGC 708
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                                                                                                                                                                                                                                                                         GIGCGCGAGGCTTTCCGTCTCGGTAICAACTTCTTCGACACCTCCCCGTATTATGGAGGA 183
                                                                                                                                                                                                                                                                                                                                                        TACATTGTGGCTACTAAGTGTGGTAGATATAAA-------GAAGGTTTTGATTTC 291
                                                                                                                                                                                                                                                                                                                                                                                                AGTGCTGAGAGAGTAAGAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTAT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                      GTTGACATACTTCATTGCCATGACATTGAGTTCGGG---TCTCTTGATCAGATTGTGAGT 408
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238 LeuSerAsnAlaGlyProGlnSerTrpHisProGlySerProGluLeuLeuAlaValGly
                                                                                                                                                                                                                                              184 ACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAAGGCTTTGCAAGTCCCTAGAAGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACAGITITAGCAAACAAGGAGATITCGTCGGGTGGTTGGGATGAGCTCTGTCTCACAG
                                                                                                                                                                                           AAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGT
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EMBL; AX118797; AAMS0657.1; -.
INTACT; Q9VGF1; -.
INTACT; QPVGF1; -.
INTERPRO; IPR001395; CG3397.
INTERPRO; IPR001395; Aldo/ket red.
Pfam; PR00248; Aldo Ket red; I.
PRINTS; PR00069; ALDKETPRASE.
SEQUENCE 342 AA; 38085 WW; D9128A46172B76B1 CRC64;
                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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                                                                                                 8.38e-34
544.50
58.75%
36.56%
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
Score:
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278 TyrThrMetGlnLeuAspGlyAlaAlaThrPheLeuIleGlyIleProAsnArgLysLeu 297
                                                                                                                                                       314 GlnGluValLeuGlnTyrLeuArgGluAsnValPheThrLysSerTyrSerTrpGlySer 333
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                                                        298 LeuargileAsnLeuaspalailePheasp-------dlyLeuThrSerHisGlu
                                                                                                                               889 CTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTA-----AAGAATCTGACATGGCCAAGT
                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIM-BAILSON N2;
MEDILINE-99069613; PubMed-9851916;
WormBase Consortium;
WormBase Consortium;
WormBase Consortium;
inventigating biology. The C. elegans Sequencing Consortium.";
sitence 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of C. elegans cosmid F37C12.";
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
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439 AA; 49696 MW; B0508EB84720FFCD CRC64;
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120
120
106
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Last sequence update)
Last annotation update)
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WormPep, F37C12.12, CE00825.
InterPro, IPR001395, Ado/ket_red.
Pfam. PF00248; Aldo ket_red.
PRINTS, PR00069, ALDKETEDTASE.
ProDom; PD000288; Aldo/ket_red, 1.
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503.00
54.60%
36.81%
30.43%
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Submitted (JAN-2003)
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SEQUENCE FROM N.A.

STATN=306 / ATCC 13902 / XV 101;

STATN=306 / ATCC 13902 / XV 101;

MEDLINE=2202145; PubMed=12024217; DOI=10.1038/4174599;

AD Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

AD Usaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

ALVES L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,

AD Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Caracili R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

Formighieri B.F., Franco M.C., Greggio C.C., Gruber A.,

Formighieri B.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Martins E.C., Machadoi M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

A pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

Spinola L.A.F., Tarkta M.A., Tamura R.E., Teixeira B.C., Tezza R.I.D.,

Setubal J.C., Kitajima J.P.,

T. "Comparison Of the genomes of two Xanthomonas pathogens with differing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------GAGTTCGGGTCTCTTGATCAG 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GGAACACTGTCTGAGAAATGCTTGGTAAGGGACTAAAAGGCTTTGCAAGTCCCTAGAAGT 240
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ValArgArgAlaPheAlaSerLeuGlyArgLeuGlyThrAspTyr1leAspValLeu
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AspTyrThrLeuSerThrLysValGlyArgCysValTyrAspAspAlaHisAlaAla
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   Proteobacteria; Gammaproteobacteria; Xanthomonadales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001395; Aldo/ket_red.
Pfam; PF00248; Aldo ket_red; I.
ProDom; PD000288; Aldo/ket_red; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          336 AA; 34982 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         host specificities.";
Nature 417:459-463(2002).
EMBL; AE012069; AAM39019.1; --
HSSP; PS2895; 1J96.
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                    Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.45e-24
426.00
50.86%
33.71%
25.77%
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                                                                            GluThrAlalleLysGlnGlyIleAsnTyrlleAspThrGlyTyrTrpTyrSerGlnSer 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ....--AlaProLysLeuTyrPheSerValAsnLeuSerIle 268
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------ThrArgAsnIleAlaValIleAsnSerGlyAla 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCAAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACA 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTGAAAGTCTGGGGATGGATCAAGAAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCT 918
                                                                                                                                                                                                    247 ATTGTGGCTACTAAGTGTGGGTAGA-----TATAAAGAAGGTTTTTGATTTCAGT 294
                                                                                                                                                                                                                                                                              GCTGAGAGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTT 354
                                                                                                                                                  |||||||
| 199 AspileCysTyrValGlnIleHisAspAlaAspPheAlaProAsnGluSerIleValLeu
127 CGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACA
                                                                                                                                                                                                                           ::::::|||||| |||||||
TyrlleSerThrLysValGlyArgPheGluLeuAspTyrAlaArgThrPheAspPheArg
                                                                                                                                                                                                                                                                                                   219 TyrGluThrLeuGlnAlaLeuGluMetAlaLysSerSerGlyLysIleArgHisIleGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         814 AGCICTGTCTCACAGGTAGAAGAAATGTT------GCAGCAGTTACAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValdiuGlnArgValArgAspArg------IleMetArgArgTyrLeuAspArg
                                                                                                                               187 CTGTCTGAGAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTAC
                                                                                                                                                                                                                                                                                                                                                     GACATA-----CTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGATTGTG---
                                                                                                                                                                                                                                                                                                                                                                                                                             406 AGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCACTGGTCTTCCGTTAGAT------ATTTTCACTTATGTTCTTGATCGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCTCCAGGGACTGTCGATGTGTTTTTGTCATACTGTTTACGGCGTTAATGATTCGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   574 TTGCTGGATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCA
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Last annotation update)
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OrderedLocusNames=XAC4184;
Xanthomonas axonopodis (pv. citri).
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LeuGluAsnAlaGlyTrp 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Q8PF04;
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08PF04
1D Q8PF0
AC Q8PF0
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DT 01-0C
DT 01-0C
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Lewis S.E.;
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  MEDLINE=20196066; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celniker S.E., Holt R.A., Bvans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.;
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Mr. H., Doyle C., Baxter B.G., Helt G., Nolson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayzaktarcglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
Cherry J.M., Cawlley S., Dabhec C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                906
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179 IleGlyLeuGlyValAmnGluGlnAspValAlaLeuGluValLeuProArgPhePro--- 197
                                                                                                                                                                                                                                                        580 GAT------TIRCTIACTIACTIACTIGAAGAGCAAAGGTGTGGGTGTGATA 621
                                                                                                                                                                                                                                                                                                                                                AGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAA---CAAGGTCCTCCTGAATGGCAC 678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGCTTCCCCT------GAGCTCAAGTCTGCAAGCCAAAGCCGCAGTTGCTCAC 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAG 786
LeuLeuHisAspIleGlyAlaLeuThrHisGlyAspAsnHisAlaAsnValLeuArgGln 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      787 GAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAAATGTTGCA
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                                                                                                                                    ATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCA
                                                                                                                                                                                                                            GGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTG
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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ORFNames=CG12224;
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A Posler C., Gabrielian A.E., Garra C., Ferinca S., Firitzbungill W., RA Durbin K.U., Brangelista C.C., Ferinca C., Gabrielian A.E., Garrell J.H., Gu Z., Guan P., Harris M., Harris M.L., Harrandez J.R., Houck J., Harrandez J.R., Houck J., Harrandez J.R., Houck J., Howland T.J., Wei M.H., Ibbegwam C., J. Houston K.A., Howland T.J., Wei M.H., Ibbegwam C., J. Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z., Land Y., Liei Y., Levitsky A.A., Li J., Li Z., McPherson D., RA Morkulov G. Milahina N.V., Mobarry C., Morris J., Moshrefi A., Ram Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Rainer K., Remington K., Saunders R.D., Scheeler F., Shen H., Rytskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Shine B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E., Sante B.C., Stapleton M., Strong R., Sun E., Mang Z.Y., Wassarman D.A., Weinsenbach J., Weissenbach J., Williams S.M., Woodaget, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., R. Zheng X.H., Zabong F.N., Zhong W., Zhon G., Zhao G., Zhao G., Zhao G., Zhao G., Zhao S., Shith H.O., R. Three R., Wang S., Zhu X., Smith H.O., R. Three R., Wang S., Zhu X., Smith H.O., R. Three R., Mang C., Zhong R., Weissenbach J., R., Myers B.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDININE-22426065; PubMed=12537568;
MEDININE-22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Facifer B.D., Kichards S., Sodergren B.J., Klahards S., Sodergren B.J., Weinsteka B., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.; Pinlahing a Whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frige B., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.B.;
"The transposable elements of the Drosophila melanogaster euchromatin:
Ferriera S., Fleischmann W.,
lbart W.M., Glasser K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22426069; PubMed=12537572;
MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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FlyBase; FBGN0037974; CG12224.
InterPro; IPR001395; Aldo/ket_red.
PRINTS; PR00069; ALDCKETROTASE.
SEQUENCE 294 AA; 32984 MM; 8B0
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SEQUENCE 335 AA; 34773 MW; 36B212C16AFA2F1F
335 AA
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PRT;
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EMBL; AB012528; AAM43286.1; -.

Interpro, IPR001395; Aldo/ket_red.

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Prodom; PD000288; Aldo/ket_red; 1.
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Gaillardin C., Weissenbach J.,
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Bouchier C., Caudron B., Scarpelli C., Mincker P., Souciet J.L.;
"Genome evolution in yeasts.";
Nature 430:35-44(2004).
EMBL. CR380525, CAG59159-1.
InterPro. IPRO1955, Aldo/ket_red.
Pfam, PP00248, Aldo ket_red, I.
PRINTS, PRO0069, ALDOERFEDTASE.
PRODOM; PD000288; Aldo/ket_red, I.
SEQUENCE 336 AA, 38209 WW; 48EBEBE
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SEQUENCE FROM N.A.

C Gendlevures

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G Gendlevures

Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,

Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,

B Barnay S., Blanchin S., Bedreich J.M., Beyne E., Bleykasten C.,

B Barnay S., Blanchin S., Eatrhead C., Ferry-Dumazet H., Groppi A.,

Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,

M Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,

Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,

Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Wirth B.,

Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
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                                                                                                               CTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTA 483
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MetalaGluLeuLysAlaAlaGlyAlaCysGlyAlaIleGlyLeuGlyValAsnGluGln 185
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                                                                                                                                                                                                                                                                                                                                                           GATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCA
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|LeuLeuSerAspAlaArgGlyProGlyAlaThrTyrAsnTyrAlaProValAspAlaAla
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                             -------GAGTTCGGGTCTCTTGATCAGATTGTGAGTGAAACAATTCCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 TACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGAT-----TTA
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                                                                                          TTGGAGAGGCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGACATT-----
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Similar to sp|O04212 Saccharomyces cerevisiae YMR041c.
ORFNames=CAGLOF06061g;
Candida glabrata CBS138;
Bukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
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ArgSerValAlaGluValGln 304
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                                                                                                                                                                                                                                                                                                                                      220 GCTTTGCAAGTCCCT-----------AGAAGTGACTACATTGTGGCT 255
                                                                                                                                                                                                                                                                                                                                                                                            ACTAAGTGTGGTAGATATAAA---GAAGGTTTTGATTTCAGTGCTGAGAAGGAAAG 312
                                                                                                                                                                                                                                                                                                                                                                                                            372
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|LeuLysGluGluGlyValIleArgHisPheGlyLeuSerGlyTyrProValLysTyrLeu 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    714
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48EEBE66D6FE682F CRC64
                                        336
1110
65
122
122
                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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886 ACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTA-------AAGAATCTG 930
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
Bospons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
A Swennene D., Tekaia F., Wesolowski-Louvel M., Westhoff E., Wirth B.,
Zeniou-Meyer M., Zivanovic I., Bolotin-Pukuhara M., Thierry A.,
Mincker P., Souciet J.L.,
Mincker P., Souciet J.L.;
I. Mature 430:35-44(2004).
                                                                                                                            GAAGAAAATGTTGCA-----GCAGTTACAGAGCTTGAAAGTCTGGGGATGGATCAAGAA
                                                                                                                                                                       TTAGCAAAC----AAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORFNames=YALIOF30811g,
Yarrowia lipolytica CLIB99.
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
5inflar to sp|004212 Saccharomyces cerevisiae YMR041c unknown
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EMBL, CR382132; CAG78880.1; -.
InterPro; IPR001395; Aldo/Ket_red.
Pfam; PF00248; Aldo ket_red; I.
PRINTS; PR00069; ALDKETRDTASE.
PRODOM; PD000289; Aldo/Ket_red; 1.
SEQUENCE 330 AA; 36474 \( \text{MW} \); 345DCDA8E7332A0D CRC64;
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Matches:
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54.55%
36.04%
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106 LysGluGlyIleArgAlaSerValGluArgSerLeuAspValLeuHisThrThrTyrAla 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGTCTCACAGGTAGAAAAATGTTGCAGCA-------GTTACAGAGCTT 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---valserThrvalGluGluLeuGlnAlaAlaLeuAspAsnTyrTrpLeuAlaLysSer 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||::
|GluSerValSer---AspGlnGluMetPheAspAsnValLysSerLeuTyrGlyAspGln 316
                                                                                                                                  238 AGTGACTACATTGTGGCTACTAAGTGTGGTAGATATAAAGAAGGT---TTTGATTTCAGT 294
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                                                                                                          82
           47
||||||| :::||||||| 68 -----SerGluVall1eLeuGlyGlyValLeuAspLysLeuLysGluLysTrpProArg
                                                                                                                                                 |||||||::::::||||||||||||||||||-----valAspIleValLeuSerTyrSerAsnMetCysLeuGlnAsnThrLeuLeuLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                               637 GCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTC
                                  124 GTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGA
                                                                                                                                                                                                                                                                                  415 ATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGT
                                                                                                                                                                                                                                                                                                                                  CTTCCGTTAGATATTTTCACTTATGTTCTTGAT-------CGAGTGCCTCCA
                                                                                                                                                                                                                                                                                                                                                                                 520 GGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTG
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                                                                                    184 ACACTGTCTGAGAAATGCTTGGTAAGGGACTAAAAGGCTTTGCAAGTC-----CCTAGA
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Search completed: November 13, 2005, 08:30:17 Job time : 122.5 secs

GGAAGTGTCTTCGGTCCAGTCGCCGAAGATGAT---------GCCGTCGCCACC 123

US-10-606-300-12 (1-960) x Q6BZU5 (1-330)

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Scoring table:

Minimum DB 8 Maximum DB 8

Searched:

Perfect score:

Sequence:

OM protein

Run on:

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Acn48848 Cotton pr
Ablo6602 Drosophil
Ablo6602 Drosophil
Ablo664 Drosophil
Ablo864 Drosophil
Abl19246 Drosophil
Abl19246 Drosophil
Ad48418 Baccerial
Aca1511 Prokaryot
Abs50132 Baccerial
Aca33777 Prokaryot
Abd1143 Pseudomon
Abd1187 Pseudomon
Ad41709 Bacterial
Aca31676 Prokaryot
Abd1187 Bifdobac
Aca21919 Prokaryot
Aca21919 Prokaryot
Aca21919 Prokaryot
Aca21919 Prokaryot
Aca2191 Prokaryot
Aca5191 Prokaryot
Aca51919 Prokaryot
Aca666 DNA Accoula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-galactose dehydrogenase; L-galDH; transgenic organism; ascorbic acid; herbicide; chromosome 4; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "L-galactose dehydrogenase (L-galDH)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana L-galactose dehydrogenase (L-galDH) cDNA
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ABL20064
ABL28814
ABL28814
ABL19246
AAG28895
ADT48436
ACA21511
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ADA00836
ADT45414
ADT44646
ADT44646
ADCA33942
ADCA33610
ADCA30666
                                                                                                                                                                                                                                                                                                                                                                                       ADS50132
ADS55648
ACA311443
ABD111443
ADT41709
ACA31676
ABS52452
AAS52452
AAS52452
AAS52452
AAS5412
AAS46119
ADS46119
ADT44628
AAS54112
ACA3112
ACA5112
ACA5112
                                                                                 ACN48848
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AAD19526
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                                                           \begin{array}{c} \textbf{1} \\ \textbf{2} \\ \textbf{3} \\ \textbf{4} \\ \textbf{5} \\ \textbf{5} \\ \textbf{6} \\ \textbf{7} \\ \textbf{
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Abk10125 A. thalia
Aac37387 Arabidope
Acn48774 Cotton pr
Ab120521 Drosophil
                                                                                                                                                                                                        November 13, 2005, 08:37:08; Search time 614 Seconds (without alignments) 3075.566 Million cell updates/sec
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1 MTKIELRALGNTGLKVSAVG......VEAILEPVKNLTWPSGIHQN 319
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                                  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                      nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4390206 seqs, 2959870667 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAD19526
ABK10125
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                              Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
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Match
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Database :

Score

Result

1619 1619 1588 779.5 593.5

220 660 240 720 260 780 280 840 300

900

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88; gene; ascorbic acid; vitamin C; scurvy; recombinant yeast; L-galactose dehydrogenase; LGDH; L-galactono-1,4-lactone dehydrogenase; ARA; D-arabinono-1,4-lactone oxidase; ALO; L-gulono-1,4-lactone oxidase; GLO; aldonolactonase; AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to generating ascorbic acid or its salt, involves obtaining a recombinant yeast capable of converting an ascorbic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GluAlaileLeuGluProValLysAsnLeuThrTrpProSerGlyIleHisGlnAsn 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661 GGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCAGGTAAGCCGCAGTT
                                                                                                                                                                                                                                                                                AlaHisCysLysSerLysGlyLysIleThrLysLeuAlaLeuGlnTyrSerLeuAla
                                                                                                                                                                                                                                                                                                             721 GCTCACTGCAAATCAAAGGGCAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                  AACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ValAlaAlaValThrGluLeuGluSerLeuGlyMetAspGlnGluThrLeuSerGluVal
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                                                                          SerLygGlyValGlyValIleSerAlaSerProLeuAlaMetGlyLeuLeuThrGluGln
                                                                                                                                                                                                                                                                                                                                                                                       AsnLysGluIleSerSerValLeuValGlyMetSerSerValSerGlnValGluGluAsn
                                                                                                                                                                              GlyProProGluTrpHisProAlaSerProGluLeuLysSerAlaSerLysAlaAlaVal
involves culturing yeast or ascorbic acid in medium id isolating ascorbic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A. thaliana cDNA encoding L-galactose dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .960
/*tag= a
/product= "LGDH"
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P-PSDB; AAU76343.
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                                                                                                                                                                                                                                                                                                The present invention relates to an isolated protein having L-galactose dehydrogenase (L-galDH) biological activity. L-galDH nucleic acid is useful for generating transgenic organisms and modified pants with enhanced ability to synthesise ascorbic acid. L-galDH facilitate the production of a plant that has been genetically modified to express a mutated L-galDH protein which is resistent to herbicides that act against the naturally occurring L-galDH and to identify and/or design compounds that are inhibitors of L-galDH and to identify and/or design compounds herbicide which acts on L-galDH and damages or kills plants that express the enzyme. The present sequence is Arabidopsis thaliana L-galactose dehydrogenase (L-galDH) CDNA. The L-galDH gene is located on chromosome 4
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                                                                                                                                                    Novel L-galactose dehydrogenase protein and nucleic acid sequence encoding the protein for producing genetically modified plants and microorganisms with enhanced ability to synthesize ascorbic acid.
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        comprishing an ascorbic acid precursor, thus forming ascorbic acid, and isolating the ascorbic acid. Also include are stabilising ascorbic acid or its salt in a medium, by culturing a yeast in a medium comprising ascorbic acid or its salt and a recombinant yeast functionally transformed with a coding region encoding a protein having an enzyme activity selected from L-galactose dehydrogenase (IGDH), L-galactono-1, 4-lactone dehydrogenase (ALD). D-arabinose dehydrogenase (ALD), D-arabinose dehydrogenase (ALD), D-arabinose dehydrogenase (ALD) activity, where the recombinant yeast is capable of converting to ascorbic acid at least about 23% ascorbic acid precursor or is capable of producing at least 20 mg ascorbic acid precursor or is capable of producing at least 20 mg ascorbic acid precursor. The ascorbic acid preduced (Witemin C) is a powerful antioxidant, a deficiency of which causes scurvy in humans. The present sequence encodes
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precursor into ascorbic acid, culturing the recombinant yeast in a medium
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                                                                                                                                                                     GCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACATTAGCA
                                                                            AsnLysGlulleSerSerValLeuValGlyMetSerSerValSerGlnValGluGluAsn
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                                                                                                781 AACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAAAT
221 GlyProProGluTrpHiBProAlaSerProGluLeuLysSerAlaSerLysAlaAlaVal
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                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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25 - MAR - 1999

26 - MAR - 1999

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20-MAY-1999;
21-MAY-1999;
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The invention relates to 17880 cotton expressed sequence tags (ESTB;
ACNA5220-ACN63099). The ESTB were isolated from cDNA libraries generated
from primed or non-primed seeds from varitety DPSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
crassies, developing fibres, carpel walls and septa from variety
Nucotton3B. The invention also relates to substantially purified
cromprising a mucleic acid of the invention. The cotton ESTB are useful as
comprising a mucleic acid of the invention. The cotton ESTB are useful as
comprising a mucleic acid of the invention. The cotton ESTB are useful as
comprising a nucleic acid of the invention. The cotton ESTB are useful as
comprising a nucleic acid of the invention. The motleic acid molecules may be
comprised with plant genetic regions, to isolate genes to mappoil can detabolic and catabolic pathways. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes are
clinks in metabolic and catabolic pathways. The nucleic acid molecules are
also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to mitigate stresses encountered
also useful for identifying genes integet stresses encountered
curing seed germination. The ESTB additionally enable the acquisition of
promoters and cis-regulatory elements which will be useful to express
comprised by permits the acquisition of molecules markers useful in
significant genes. The nucleic acid molecules are further useful for
detecting the expression level or pattern of a protein or mikha and for
detecting the presence or quantity of a protein or mikha and for
detecting the presence or quantity of a protein or mikha protein or present
cotton variety DPSOB primed seed cDNA library (LiBisd25). The sequence
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New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 3555; 34pp; English.

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Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety DPSOB; library LIBS825; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; se.
                                                                                                                                                                                                                                                  Cotton primed seed EST Clone ID: LIB3825-027-Q6-K6-G2, SEQ:3555
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                                                                                                                              BP.
                                                                                                                              ACN48774 standard; cDNA; 564
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FENG P C C.
FINCHER K L.
ZIEGLER T E.
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                                                                                                                                                                                  GACAAATGTGGGAGATATCGTGAAGGTTTTTGATTTTCAGTGCTGAGAGAGTAACTAAAAGC
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                                                                                                                                                                                                                                                                                                  TyrValLeuAspArgValProProGlyThrValAspVallleLeuSerTyrCysHisTyr
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data for this patent did not form part of the printed specification, was obtained in electronic format directly from the US patent office segdata.uspto.gov/sequence.html?DocID=US20040123340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ds.
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                                 Sequence 564 BP; 156 A; 97 C; 135 G; 175 T; 0 U; 1 Other;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                   1.05e-73
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                                                                  220 nGlyProProGluTrpHisProAlaSerProGluLeuLysSerAlaSerLysAlaAlaVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaSerProteuGlySerValPheGly---ProValAlaGluAspAspAlaValAlaThr
                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 37945.
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                                     BP.
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          824/c
ABL28824 standard; DNA; 3308
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517.00
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                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                            pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP NY
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Query Match:
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                                                                                                                                                                 26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2166
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ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DPSOB, mature seeds from
covariety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety
CC from primed or the fragments encoded by nucleic acid molecules of the
covariety coker stansformed plants having a nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTs are useful as
cc invention, and to transformed plants having a nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTs are useful as
cc offer isolate genetic regions, to isolate genes to members of a particular gene family. The nucleic acid molecules may be
cc used for isolating avariety of agronomically significant genes
cc used for isolating avariety of agronomically significant genes
cc associated with plant growth, quality, yield, and could also serve as
links in metabolic and catabolic pathways. The nucleic acid molecules are
calso useful for identifying genes important in initiating and maintaining
cc also useful for identifying genes important in initiating and maintaining
seed germination or that may be used to mitigate stresses encountered
during seed germination. The ESTs additionally enable the acquisition of
cypromociers and cis-regulatory elements which will be useful to express
contromically significant genes in these tissues and/or other tissues,
and also permits the acquisition of molecular markers useful for
cetecting the expression level or pattern of a protein or mRNA and for
detecting the expression level or pattern of a protein or warder for
cotton variety DPSOB primed seed colland EST isolated from a
cotton variety DPSOB primed seed colland and a protein or printed sequence
cc data for this patent did not formet disamples of the printed specification or expression level or pattern of the printed specification or expression lev
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                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTATTGCCTTACTTGAAAACCAAAGGTGTTGGCGTAATCAGTGCATCTCCACTTGCTATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 563 BP, 157 A; 126 C; 112 G; 168 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                               Fincher KL,
                     12-DEC-2001; 2001US-00021323.
                                                                            14-DEC-2000; 2000US-0255619P
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497.00
88.00%
77.60%
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                                                                                                                           DEIXMAN J.
FENG P C C.
FINCHER K L.
ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                   WPI; 2004-479808/45.
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                                                                                                                                                      (FENG/)
(FINC/)
(ZIEG/)
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274
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                                                                                                                                                                          275 SerGinValGluGluAsnValAlaAlaValThrGluLeuGluSerLeuGlyMetAspGln 294
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                                                                                                                                                                                                                                                                                                                        202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABILG176-ABI3051), expressed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                        GluThrLeuSerGluValGluAlaIleLeuGluProValLysAsnLeuThrTrpProSer
                                                                                                                                                                                                                                                                                                      GAAACTCTAGCTGAGGTGGAAGCAATACTGAAGCCAGTGAAGAATCAGACATGGCGGAGC
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                                                                            255 LeuGlnTyrSerLeuAlaAsnLysGluIleSerSerValLeuValGlyMetSerSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster expressed polynucleotide SEQ ID NO 14288.
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11-JUL-2000; 2000US-00614150
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458.00
54.30%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIA1575, ABIA30511), expressed DNA sequences (ABIA16175) and the encoded proteins (ABB57737 ABB7072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                               Drosophila melanogaster expressed polynucleotide SEQ ID NO 14291
                                                                                                                                                                                                                                                                                                     developmental biology; cell signalling; insecticide,
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                                                             ABL06603 standard; cDNA; 885 BP.
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pharmaceutical; gene; ss.
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P-PSDB; ABB62500
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CTCGGTGCCTTCCTGCAGACC-----AAGCGGCGACGAGAGTTCGTCTGTGTCACCAAG 252
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| AAGGTGCGGCCGAGGGCGTCGTATCGGCATCGGCATCGATGGTGTCGGATGCC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 PheThrTyrValLeuAspArgValProProGlyThrValAspValljeLeuSerTyrCys 183
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                                                                                           Novel L-fucose dehydrogenase gene - a new recombinant DNA and the prepn of L-FDH using a L-FDH vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          313 GACTICCACGIGCCCGACGACGACCGCGAGTGGGACTICCACCGAGCAGGCATCGT
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                                                                                                                                                    The L-FDH gene is new and can be used for the recombinant prodn. enzyme. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                       Sequence 987 BP; 140 A; 371 C; 340 G; 136 T; 0 U; 0 Other;
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Matches:
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                                   KAGAKU KENKYUSHO
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                                                                                                                               Claim 1; Page 4-5; 6pp; Japanese.
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P-PSDB; AAR51284.
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11-SEP-1992;
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                                                                                                                                                                                                                                                                                                                            Sequence 10418 BP; 2894 A; 2143 C; 2343 G; 3038 T; 0 U; 0 Other;
                                                                                                                                        Claim 1; SEQ ID NO 37915; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                   10418
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                           Venter JC, Adams M,
                                                       WPI; 2001-656860/75
CORP NY
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(PEKE)
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1615-AB130511), expressed DNA aequences (ABL16157) and the encoded proteins (ABB57137-ABB72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValArgGluAlaPheArgLeuGlyIleAsnPhePheAspThrSerProTyrTyrGlyGly 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 AlaSerProLeuGlySerValPheGly---ProValAlaGluAspAspAlaValAlaThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10451 BP; 2904 A; 2145 C; 2346 G; 3056 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                              developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 9211.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 9211; 21pp + Sequence Listing; English.
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CTACGATGTGGACGTGCTGAAGGAGTGTGCCGAGCGG
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ABL19246 standard; DNA; 10451
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75.
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Best Local Similarity:
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Pred. No.:
                                                                                                                                                                                                                                                                  Drosophila;
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  28
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                                                                                                                                  ABL19246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472
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DB:
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533

41

Search completed: November 13, 2005, 08:51:32 Job time : 636 secs

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Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

**BLOSUM62** 

Scoring table:

US-10-606-300-11

Title: Perfect score:

Sequence:

protein

Run on:

seq length: 0 seq length: 200000000

Total number Minimum DB E Maximum DB E

Searched:

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120
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114964, Ap
114964, Ap
114787, A
20, Appl
20, Appl
20, Appl
2318, Appl
1263, Ap
1263, Ap
2515, Ap
2515, Ap
2558, Ap
2568, Ap
2568, Ap
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5370, Ap
24, Appl
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Sequence 2568,
Sequence 2169,
Sequence 3767,
Sequence 1183,
Sequence 1264,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGACGAAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGGGCGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheGlyAlaSerProLeuGlySerValPheGlyProValAlaGluAspAspAlaValAla
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; Patent No. 6630330
; GENERAL INFORMATION:
; APPLICANT: Sauer, Michael
; TITLE OF INVENTYON: Ascorbic Acid Production from Yeast; FILE REFERENCE: 2028.594000
; CURRENT APPLICATION NUMBER: US/09/630,983A
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               960
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             US-09-710-279-3821

US-09-673-198-9

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US-09-902-54-716

US-09-902-54-716

US-09-902-54-716

US-08-920-812-20

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US-08-920-812-20

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ORGANISM: Arabidopsis thallana
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DB:
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-MODEL=frame+ p2n.model -DEV=xlh
-C-Graz 1/USPTO spool h/US10606300/runat 07112005 094939 8202/app query.fasta_1.455
-D=L-GGRZ_1/USPTO spool h/US10606300/runat 07112005 094939 8202/app query.fasta_1.455
-D=LSBaued Patents NA -OFMT=fastap -SUFFIX=p2n.rni -MINNATCH=0.1 -LOOPEL=0
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Sequence 10047, A
Sequence 3178, Ap
Sequence 1145, Ap
Sequence 1145, Ap
Sequence 13505, A
Sequence 13948, A
Sequence 1166, Ap
Sequence 2323, Ap
Sequence 3237, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Appl
Sequence 3, Appli
Sequence 10047, A
                                                                                                                                          November 13, 2005, 08:39:29; Search time 208 Seconds (without alignments) 2509.482 Million cell updates/sec
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                     GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-630-983A-12
US-07-855-793-3
US-09-252-991A-10047
US-09-252-991A-10047
US-09-902-540-3178
US-09-902-540-1145
US-09-252-991A-13905
US-09-252-991A-13905
US-09-902-540-3489
US-09-902-540-3489
US-09-107-522A-3237
US-09-107-522A-3237
                                                                                                    nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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20

В Length

Query Match 1

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Result

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2682 1104 2514 1044 1026 1515 1999 17188

1619 351.5 317.5 314.5 314.5 302.5 300.5 296.5

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Matches:
Conservative:
Mismatches:
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 KD
COMPUTER: Diskette, 5.25 inch, 500 KD
COMPUTER: TBM COMPACTION
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/855,793
FILING DATE: 19920323
CLASSIFICATION 435
FILING DATE: 19920323
CLASSIFICATION NUMBER: ATTORNEY
APPLICATION NUMBER: ATTORNEY MATE: WATEN M. Check Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INPORMATION:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "844-1809 |
PUBLICATION INFORMATION:
TITLE:
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 2682 Base Pairs TYPE: UNCLEIC ACID STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: genomic DNA HYPOTHETICAL: FRAGMENT TYPE: CRIGINAL SOURCE:
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INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
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CHROMOSOME/SEGMENT:
MAP POSITION:
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Best Local Similarity:
Query Match:
DB:
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TISSUE TYPE:
CELL TYPE:
CELL LINE:
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VOLUME:
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1 Sequence 3, Application US/07855793

2 Sequence 3, Application US/07855793

3 Sequence 3, Application US/07855793

3 Patent NO. 5217800

3 TILLE OF INVENTION: HITTA et al.

4 TILLE OF INVENTION: DEHYDROGENASE GENE,

7 TILLE OF INVENTION: DEHYDROGENASE BY THE USE OF SAID MICROORGANISM

7 TILLE OF INVENTION: DEHYDROGENASE BY THE USE OF SAID MICROORGANISM

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                                                                                                                             GlyThrLeuSerGluLysMetLeuGlyLysGlyLeuLysAlaLeuGlnValProArgSer
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               ThrValArgGluAlaPheArgLeuGlyIleAsnPhePheAspThrSerProTyrTyrGly
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                                                                                                                                                                                                                                                                                                                                                                                      ProLeuAspIlePheThrTyrValLeuAspArgValProProGlyThrValAspValIle 179
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                               64
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                                                         ProLeuGlySerValPheGlyProValAlaGluAspAspAlaValAlaThrValArgGlu 44
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                   GluLeuArgAlaLeuGlyAsnThrGlyLeuLysValSerAlaValGlyPheGlyAlaSer
                                                                                                                                        GluLysMetLeuGlyLysGlyLeuLysAlaLeuGlnValProArgSerAspTyrIleVal
                                                                                                                                                                                AlaThriyeCysGlyArgTyr-----LysGlu
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US-10-606-300-11 (1-319) x US-07-855-793-3
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US-09-252-991A-10047
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Sequence 10047, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
TYPLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
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Matches:
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Indels:
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ORGANISM: Pseudomonas aeruginosa
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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxcoccus xanthus Genome Sequences and Uses Thereof FILE REPERBNCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
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                                                            132 AspGlnIleValSerGluThrIleProAlaLeuGlnLysLeuLysGlnGluGlyLysThr
                                                                                                                        152 ArgPhelleGlylleThrGlyLeuProLeuAspIlePheThrTyrValLeuAspArgVal
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US-09-902-540-3178
; Sequence 3178, Application US/09902540
; Patent No. 6833447
; Extent No. 7 TREADMATTON:
 120 IleLeuHisCysHisAspIle----
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SEQ ID NO 3178
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Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR SEQ ID NOS: 33142
SEQ ID NOS: 33142
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               SerProLeuAlaMetGlyLeuLeuThrGluGlnGlyProProGluTrpHisProAlaSer 229
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Batent No. 683347

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
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6081 GTGGCCATTGGCAATGGCTTCGCGTCCACCGACGCGCAGGCGCAGGCCACCTTGAAG 6022
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Matches:
Conservative:
Mismatches:
Indels:
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEG ID NO 1145
LENGTH: 14382
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314.50
45.74%
26.70%
19.43%
                                                                                                                                                            TYPE: DNA ORGANISM: Myxococcus xanthus
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Best Local Similarity:
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DB:
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226 HisProhlaSerProGluLeuLysSerAlaSerLysAlaAlaValAlaHis 242	RESULT 7 US-09-252-991A-13505 Sequence 13505, Application US/09252991A Sequence 13505, Application US/09252991A Sequence 13505, Application US/09252991A Sequence 13505, Application US/09252991A TITLE OF INVENTION: TITLE OF INVENTION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 13505 LENGTH: 1026 LENGTH: 1026 TYPE: DAA ORGANISM: Pseudomonas aeruginosa	1026   2.98-27   Length: 1026   Matches: 30.50   Matches: 94   Sonscraptive: 36.50   Matches: 94   Sonscraptive: 58   Mismatches: 127   Indels: 127   Indels: 127   Indels: 127   Indels: 127   Indels: 127   Indels: 11   Indels: In	Qy         86 ThrLys

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APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: State, Steven C.
APPLICANT: State, Steven C.
APPLICANT: Wiegend, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPREBRUE: 38-10[15849]B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 3489
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                   ; Sequence 3489, Application US/09902540; Patent No. 6833447; GENERAL INFORMATION:
531 ACGCTGGAGGCGCCGCTC 514
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     Conservative:
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Indels:
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Sequence 3237, Application US/09107532A
; Patent No. 6583275
; CENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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63 LeuSerGluLysMetLeuGlyLysGlyLeuLysAlaLeuGlnValProArgSerAspTyr
                                                          --CysGlyArgTyrLysGluGlyPheAspPheSer
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
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STATE: Massachusetts
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COMPUTER READABLE FORM:
                                                             83 IleValAlaThrLys.
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Sequence 1166, Application US/09902540

Patent No. 633447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: APPLICANT: Ateven C.
TILLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof;
FILE REFRENCE: 38-10(1549)B

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2001-07-10

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1166

SEQ ID NO 1166
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                                         526 ACGTTAGAA-----CAATTGAAAGAAGCGAATGCAGATGGATATGTCGATGTAGTA
                                                                                                                                                                                              GAAGATAAATACAGTTTGATCCATCGGCAGGCTGAAAAA-------GAATTATTC
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745. AGAAATCCAGATTTCCAAGGAGAAACGTTTCAGAGAAATTTTAACCGCTGT-CGATGTACT
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                                                                                          160 ProceuAspIlePheThrTyrValLeuAspArgValProProGlyThrValAspVallle
                                                                                                                                                                                                                               ProTyrLeuLysSerLysGlyValGlyValIleSerAlaSerProLeuAlaMetGlyLeu
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                       ProAlaLeuGlnLysLeuLysGlnGluGlyLysThrArgPhelleGlyIleThrGlyLeu
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US-09-328-352-1953
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GAAATAAGA---ATCGGACATTCACAAGTCTACGCAGAACAGCTTGGATTAGGAGCAAAT 114
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GTCATCGCTACAAAAGCTGCTCATGTACCAAATAAAGGGGGAACATTTGATAATTCTCCT 354
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Matches:
Conservative:
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MEDIUM TYPE: CD/ROM 1S09660
COMPUTER: PC
COMPATAING SYSTEM: «Unknown»
SOFFWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: JA MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JA MAY 1998
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                         NAME: Atiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEPRAX: (781)893-5007
INFORMATION FOR SEQ ID NO: 3277:
SEQUENCE CHARACTERISTICS:
LENGTH: 999 base pairs
TEMPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc feature
; LOCATION: (B) LÖCATION 1...999
; SEQUENCE DESCRIPTION: SEQ ID NO: 3237;
US-09-107-532A-3237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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Sequence 1953, Application US/09328352

Patent No. 6662958

Patent No. 6662958

Patent No. 6662958

TERMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

PILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 1953
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Matches:
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             TGCATGGGAATGAGCTTTGCCTATGGTGCCTCAGACGACACACAAGCATTGCAATTGTA 120
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                                                                                                                                                                GCAAACGAAGTTTTGCTCTCA-----AAAGTTTTTAGAAAAAATCGTGACAAAGTG 231
                                               ArgGluAlaPheArgLeuGlyIleAsnPhePheAspThrSerProTyrTyrGlyGlyThr 62
                                                             292 TTAGAGTCTTATATCGACGGCTCGCCTGAGTGGATTAAAGTTGCGGTCGAAAAACGTTA
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TCGCTACTTACCCGTGAGTTTGAACAAACCCATTTGCAAACCATTCGTGAGTTAGGTATT
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US-09-134-001C-289
Sequence 289, Application US/09134001C
Parent No. 6380370
GENERAL INFORMATION:
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PELICATION NUMBER: US 60/064,964
PRIOR PELICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 289
LENGTH: 945
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------AAAAAAGGGAACCAATTATTGAAAGTGCAATTGATAATGGTATTACG
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Matches:
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                                                                                                                                                                      TYPE: DNA; CRGANISM: Staphylococcus epidermidis US-09-134-001C-289
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APPLICANT: MIYAKE, Koichiro; HASHIMOTO, Shinichi; MOTOYAMA Hiroaki;
APPLICANT: OZAKI, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji
TITLE OF INVENTION: A process for producing isopremoid compounds by
TITLE OF INVENTION: microorganism and a method for screening compounds with
TITLE OF INVENTION: antibiotic or weeding activity
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/09/673,198
CURRENT APPLICATION NUMBER: US98/103101
PRIOR APPLICATION NUMBER: J998/103101
PRIOR APPLICATION NUMBER: J998/221910
PRIOR APPLICATION NUMBER: J999-00-15
PRIOR APPLICATION NUMBER: J999-00-5
PRIOR APPLICATION NUMBER: J999-00-15
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|S00 TATCTTAAAAT-----AGTCAAATTGAAACACTTATGTCC-----CAGTTTAAT 1456
                                                                                                                                                                                                                                                                                                                                                                                                      1395 CTAGCACGTGGCCCTGTATTTAAAGGTTTAATTTAACTTCAAAAAGTGTTGATGTTATAGAT 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 GlnGluGlyLysThrArgPhelleGlyIleThrGlyLeuProLeuAspIlePheThrTyr 166
                                                                                                                                                                                                   167 ValieuAspArgValProProGlyThrValAspValIleLeuSerTyrCysHisTyrGly 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              236 SerLysAlaAlaValAlaHisCysLysSerLysGlyLysLysIleThrLysLeuAlaLeu 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            256 GlnTyrSerLeuAlaAsnLysGluIleSerSerValLeuValGlyMetSerSerValSer 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GluGlnGlyProProGluTrpHisProAlaSerProGluLeuLysSerAla
  1671 AAGGGATCATTGAAACGATTAGGATTAAACCATTTAGACTTATATCAATTACATGGC---
                                                                                                                                            187 ValAsnAspSerThrLeuLeuAspLeuLeuProTyrLeuLysSerLysGlyValGlyVal
                                       127 GluPheGlySerLeuAspGlnIleValSerGluThrIleProAlaLeuGlnLysLeuLys
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Patent No. 6806076
GENERAL INFORMATION:
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SOFTWARE: Patentin Ver. 2
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: CDS
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US-09-673-198-9
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TTAAAAAATATCAA---AATCGTGATGACATCGTTATCGGAACTAAAGTTGGAAATCGA 1732
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  726
                                                                                                                       GlnTyrSerLeuAlaAsnLysGluIleSerSerValLeuValGlyMetSerSerValSer 275
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                                                                                                                                                                                                   GlnValGluGluAsnValAlaAlaValThrGluLeuGluSerLeuGlyMetAspGlnGlu 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3821
LENGTH: 2993
                                                               :::||| |||:::
-----ACGATTGCTTCTATTAAAGAATTGGAAAGTAATTTAACCGCGTTATCATTT
                                                                                                                                            676 GAAAAATTTAAAAACGGTGTGTTAGATTAC----ACTCAAGACGAATTAGGTAGC---
                                       SerLysAlaAlaValAlaHisCysLysSerLysGlyLysLysIleThrLysLeuAlaLeu
                                                                                                                                                                                                                                                                                 296 ThrLeuSerGluValGluAlaIleLeuGluProValLygAsnLeuThrTrp 312
                                                                                                                                                                                                                                                                                                            Description of Artificial Sequence: synthetic nucleic acid sequence
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Patent No. 6703492
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ORGANISM: Artificial Sequence
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OTHER INFORMATION:
US-09-710-279-3821
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Best Local Similarity:
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US-10-606-	300-11 (1-3	19) x US-09-673-	198-9 (1-1044)		
ර් සි	4 IleGluL	eGluLeuArgAlaLeuGlyAsnThrGlyLeuLysValS ::::                GCAATACAACCCTTAGGAAAAACCGACCTTCGCGTTT	ThrGlyLeuLysVals	erAla        CCGACTTTGCCTCGGCTGT	18 132
ζ	19 ValGlyP	heGlyAlaSerProLe	ıĞİYSerValPheGlyE		38
QQ	133 ATGACCT	 TTGGCGAGCCAGATCG	:::  GGTAATCACGCATGGA	ي	192
ò	39 ValAlaT	hrValArgGluAlaPhe	ArgLeuGlylleAsnE	ValAlaThrValArgGluAlaPheArgLeuGlyIleAsnPhePheAspThrSerProTyr	58
qq	193 CGICCCA	TAATTAAACGTGCACTC	<b>3GAAGGCGGCATAAAT</b> 1		252
රු සි	59 TyrGlyG     253 TATTCTG	lyThrLeuSerGluLy:       :: acgcagcagcGaaga	<pre>MetLeuGlyLysGlyI :::::   ::: JATCGTCGGTCGCGCAC</pre>	TyrGlyGlyThrLeuSerGluLysMetLeuGlyLysGlyLeuLysAlaLeuGlnValPro	78 309
δ	79 ArgSerA	SpTyrlleValAlaTh	CLV8	rgSerAspTyrIleValAlaThrLysCysGlyArgTyrLysGluGly	94
QQ	310 CGTGAAG	ACGTGGTCGTTGCGAC	CAAAGTGTTCCATCGCC	TTGGTGATTTACCGGAAGGA	369
λo :	10	heSerAlaGluArgVa	ArgLysSerIleAspC 		н :
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oy Oy	115 LeuAspT :::     424 ATGGATT	yrValaspileLeuHit                   ArGrCGATATCCTGCA	SCYBHIBABDIleGluI 	LeuaspTyrValaspIleLeuHisCysHisAspIleGluPheGlySerLeuAspGlnIle :::	134 474
ò	135 ValSerĢ	luThrileProAlaLe	GlnLysLeuLysGlnC	iluglyLysThrArgPheile	154
Ωp	475 ATCGAAG		::: :aacgacgiggiaaaa	:::	534
ζ	155 Gly1leT	GlylleThrGlyLeuProLeuAspllePheThrTyrValLeuAsp-	ollePheThrTyrVall		173
ор	535 éééecer	CATCAATGCACGCTTC	scagirigereaggead	ACTCC	594
ò :	<b>5</b> 0*	GlyThrValAspValIleLeuSerTyrCysHisTyrGly     	CTyrCysHisTyrGly-	ValAsnAspSerThrLeu	9 (
đ	ın	CGCAGTTTGTCAGTAT	SCAGGATCACTACAATO	GGCTGGGCGCAGTTTGTCAGTATGCAGGATCACTACAATCTGATTTATCGTGAAGAGAG	654
čo i	e	euLeuProTyrLeuLy:	sSerLysGlyvalGlyv	LeudapLeuLeuProTyrLeuLysSerLysGlyValGlyVal11eSerAlaSerProLeu :::::::        ::::::	212
g ;	655 CGCGAGA	CGAGAIGCTACCACIGIGITAICAGGAGGCGIGGCGGGAAITCC	rcaggaggggggggggggggggggggggggggggggggg		714
5 A	3=B		[       	CCGTGGGGAGAACTACCGCACGACTG	9
ζ	233 LysSer-			AlaSerLysAlaAlaVal	240
qq	763 GTGTCTG	atgaggtggggaaaaa	rctctataaagaaagcc	 GTGTCTGATGAGGTGGGGAAAATCTCTATAAAGAAAGCGATGAAAATGACGCGCAGATC	822
È	241 AlaHis-	Cy	SLYSSerLysGlyLys1	CysLysSerLysGlyLysLysIleThrLysLeuAlaLeu	255
οp	823 GCAGAGC	GGTTAACAGGCGTCAG	reaagaactggggggg		882
<i>\</i> 0	256 GlnTyrS	GlnTyrSerLeuAlaAsnLysGlulleSerSerValLeuValGlyMetS	IlleSerSerValLeuV	/alGlyMetSerSerValSer	275
qq	ввз ссстест	TGTTGAGTAAACCGGG	CATTGCCGCACCGATT	GCCTGCTTGTTGAGTAAACCGGGCATTGCCGCACCGATTATCGGAACTTCGCGCGAAGAA	942
<i>\</i> 6	92	luGluAsnValAlaAla	avalThrGluLeuGlu£  {	GlnValGluGluAenValAlaAlaValThrGluLeuGluSerLeuGlyMetAepGlnGlu	6
ф	943 CAGCTTG	ATGAGCTATTGAACGC	3ĠŤĠC	GATATCACTTTGAAGCCGGAA	066

aller	991 CAGATTGCCGAACTGGAAACGCCGTATAAACCG 1023	
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Search completed: November 13, 2005, 11:18:40 Job time : 231 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 13, 2005, 08:41:00; Search time 894 Seconds
(without alignments)
2950.864 Million cell updates/sec
Title: US-10-606-300-11
Perfect score: 1619
Sequence: 1 MTKIELRALGNTGLKVSAVG......VBAILEPVKNLTWPSGIHQN 319
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Scoring table: BLOSUM62
Scoring table: Xgapot 10.0, Xgapoxt 0.5
Ygapop 10.0, Ygapoxt 7.0
Pelop 6.0, Peloxt 7.0
Belop 6.0, Delext 7.0
Searched: 9794790 seqs, 4134909567 residues
Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Command line parameters:

Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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3	27		n	19	-10-424-599-1194	nce 11946
4	121		9	50	10-437-963-1145	ance 11457,
20 4			1715	21	-10-425-1	nce
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3.6	•		ľ	18	-10-282-122A-195	19546,
35	н		2256646		US-10-470-565-1	e 1, A
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41	31		933	18	S-10-282-122A-936	quence 9361,
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43	. 20	٠.	933	18	-10-369-493-4306	quence 43066,
4.4	•	18.9	999	18	10-282-122A-387	nence 38764,
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, PRIC	PRIOR APPLICATION NUM	ATION P	1 NUMBER:	8	1007651.3	
, NUMBER	ER OF SEO	O ID NO	JS: 7	1		
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Indels:
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; APPLICANT: Porror.
; APPLICANT: Porror.
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; CURRENT FILING DATE: 2003-06-25
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
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Mismatches:
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/FEY: CDS
LOCATION: (1). (960)
OTHER INFORMATION:
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Percent Similarity:
Best Local Similarity:
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Publication No. US20040123343A1

Publication No. US20040123343A1

SUBJICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei

APPLICANT: Wi, Wei

APPLICANT: Wi, Wei

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963
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US-10-424-599-119463
US-10-424-599-119463
i Sequence 119463, Application US/10424599
i Publication No. US20040031072A1
i GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: APPLICANT: Cao Yongwei
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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ITILE OF UNINERTION: Plants and Uses Thereof for Plant Improvement
ITILE OF UNINERTION NUMBER: US/10/424,599
ICURRENT APPLICATION NUMBER: US/10/424,599
ICURRENT PAILNG DATE: 2003-04-28
ISEQ ID NOS: 285684
ISEQ ID NOS: 285684
ISEQ ID NOS: 285684
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Gaps:
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US-10-424-599-119463
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1279.00
88.40%
76.80%
79.00%
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Best Local Similarity:
Query Match:
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Publication No. US/20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: 38-21 (5322)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 95-235
LIENGTH: 1715
                                    1188 GCAATTGAATTGTCTACTTCCGGTATTGATAAAGAACTTCTGCACGAAGTTGAAGCAATT 1247
  1128 ATTTCCACGGTTCTTGTTGGAATGAACTCTCCAGAACAGGTAGAGGAGAATGTGGCTGCT 1187
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                        ValThrGluLeuGluSerLeuGlyMetAspGlnGluThrLeuSerGluValGluAlaIle
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Mismatches:
Indels:
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Matches:
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1208.50
83.86%
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CTHER INFORMATION:
US-10-425-115-95235
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Zea mays
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                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
                                     ; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_17680C.1
US-10-437-963-11457
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1213.00
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  NOS: 204966
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SEQ ID NO 11457
LENGTH: 1616
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; Sequence 95234, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION: Thomas J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihna
; APPLICANT: Zhou, Yihna
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules ai
; TITLE OF INVENTION: Plants
; TITLE OF INVENTION: Plants
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 95234
        GlualaPheArgLeuGlyIleAsnPhePheAsp?
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US-10-425-115-95234
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Publication No. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 13219
LENGTH: 1434
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                   CysLysSerIysGlyLysLysIleThrLysLeuAlaLeuGlnTyrSerLeuAlaAsnLys
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CAGAAGATCAAGGAGAATGGGAAGGCACGGTTCATTGGCATCACCGGGTTGCCTCTCAGC
                                                                 CysHisTyrGlyValAsnAspSerThrLeuLeuAspLeuLeuProTyrLeuLysSerLys
                                                                                                              GlyValGlyValIleSerAlaSerProLeuAlaMetGlyLeuLeuThrGluGlnGlyPro
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OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUSS9142_1
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Matches:
Conservative:
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Best Local Similarity:
Query Match:
DB:
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US-10-767-701-13219
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Percent Similarity:
Best Local Similarity:
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US-10-425-114-31543
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ORGANISM: Zea mays
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US-10-425-114-31543
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Pred. No.:
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                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                    FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_186845C.1
        TYPE: DNA
ORGANISM: Zea mays
FEATURE:
LOCATION: (1)..(1295)
OTHER INFORMATION: unsure at all n locations
                                                                                                                       4.55e-124
1191.50
80.98%
72.39%
                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                          US-10-425-115-95234
                                                                                                              Alignment Scores:
LENGTH: 1295
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Sequence 31543, Application US/10425114

publication No. US2004003488A1

GENERAL INCORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Steen, Steven E

APPLICANT: Tabaska, Jack B

APPLICANT: Tabaska, Jack 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PhelledlylleThrGlyLeuProLeuAspIlePheThrTyrValLeuAspArgValPro 172
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                                             AspGlnGluThrLeuSerGluValGluAlaIleLeuGluProValLysAsnLeuThrTrp
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240 AAGGAAGCAGGAAATTCGTTTCATTGGTATCACCGGGTTGCCCTTGGAAATTTTTACT
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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US-11-097-143-2802
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Publication No. US20040123340A1

GENERAL INFORMATION:

APPLICANT: Delkman, Jill

APPLICANT: Feng, Paul C.C.

APPLICANT: Feng, Paul C.C.

APPLICANT: Pincher, Karen L.

APPLICANT: Pincher, Karen L.

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Number: US/10/021,323

CURRENT FILING DATE: 2000-12-14

PRIOR FILING DATE: 2000-12-14

NUMBER OF SEQ ID NOS: 17880

SEQ ID NO 3555
                                                                                                                                                                                                                                                              LeuAlaLeuGlnTyrSerLeuAlaAsnLysGluIleSerSerValLeuValGlyMetSer 272
                                                                                                                                                                                                                                                                                                                                SerValSerGlnValGluGluAsnValAlaAlaValThrGluLeuGluSerLeuGlyMet 292
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309 GITGAICTGCICCCCTACTIGAAGAGCAAAGGIGITGGGGTTAICAGIGCTICGCCCCTC 368
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COTHER INFORMATION: unsure at all n locations
COTHER INFORMATION: Clone ID: LIB3825-027-Q6-K6-G2
US-10-021-323-3355
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ORGANISM: Gossypium hirsutum
FEATURE:
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US-10-021-323-3555
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                                                                                                                                                                                                                                                                                      158 GlyLeuProLeuAspIlePheThrTyrValLeuAspArgValProProGlyThrValAsp 177
                                                                                                                                                                                                                                                                                                                                                                                        ThrGluGlnGlyProProGluTrpHisProAlaSerProGluLeuLysSerAlaSerLys 237
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                                                                                                                                                                                                            AlaGluArgValArgLysSerIleAspGluSerLeuGluArgLeuGlnLeuAspTyrVal
                                                                                                                                                                                                                    198 TyrLeuLysSerLysGlyValGlyValIleSerAlaSerProLeuAaMetGlyLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AlaAlaValAlaHisCysLysSerLysGlyLysLysIleThrLysLeuAlaLeuGlnTyr
                                         3 LysileGluLeuArgAlaLeuGlyAsnThrGlyLeuLysValSerAlaValGlyPheGly
                                                                          23 AlaSerProLeuGlySerValPheGlyProValAlaGluAspAspAlaValAlaThrVal
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                       US-10-606-300-11 (1-319) x US-11-097-143-28022 (1-1038)
Indels:
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8-11-097-143-28021/c
; Sequence 28021, Application US/11097143
; Publication No. US20050208558A1
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2604 GGCGGCGCCCTGTGCGCGAACTACGGGTAAGAGAAATCTTAACAAATTCAATTACTCCCG 2545
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APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT PILING DATE: 1099-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-28
PRIOR PRILING DATE: 1999-10-28
PRIOR PRILING DATE: 1999-11-13
PRIOR PILING DATE: 1999-11-28
PRIOR PILING DATE: 1999-11-28
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PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
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PRIOR PILING DATE: 2000-01-37
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 28021
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Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version .
SEQ ID NO 40478
LENGTH: 1051
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APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION XIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DRASOPHILA GENES.

TITLE OF INVENTION: DRASOPHILA GENES.

TITLE OF INVENTION: DRASOPHILA GENES.

FILE REFREENCE: CLOOO728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR PLING DATE: 1999-10-29

PRIOR PLING DATE: 1999-10-29

PRIOR PLING DATE: 1999-11-12

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-24

PRIOR FILING DATE: 2000-01-24
      2250 CGCCACGAAAGTGGCTCGCTACGAACTGGACTACGATAAAATGTTTGACTTTAGTGCCAA 2191
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|953 TTTATAGCATACACTTCAAATTTCAAGTTTTAAATCTCATATCGCCCACCAGACGGTCCT
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                                                          uArgValArgLysSerIleAspGluSerLeuGluArgLeuGlnLeuAspTyrValAspIl
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Sequence 3629, Application US/10021323
Publication No. US20040123340A1
GENERAL INFORMATION:
APPLICANT: Deikman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Paul C.C.
APPLICANT: Tincher, Karen L.
APPLICANT: Tincher, Karen L.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(52274)B
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
PRIOR FILING DATE: 2006-12-14
                                                                                                                                                      1692 CTACGATGTGGACGTGCTGAAGGAGTGTCGCGAGCGG---GGCAAAGGTCGCATCCAGGT 1636
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1872 GTGGACGTACTACAGGTGTTTGGTATACCAATATATAGATTTGTCTATAAACTAACAC 1813
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                         --GluGlyPheAspPhe 97
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SEQ ID NO 3629
LENGTH: 563
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US-LI-097-143-40477.

Sequence 4047, Application US/11097143

Publication No. US200502085581

Fublication No. US200502085581

APPLICANT: Vertex.

APPLICANT: Vertex.

APPLICANT: Vertex.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CL000728

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CL000728

FILE REPLIANTON: DATE: 1999-10-03

PRIOR FILING DATE: 1999-10-19

PRIOR PLILING DATE: 1999-11-12

PRIOR PELICATION NUMBER: 60/161,932

PRIOR PELING DATE: 1999-11-12

PRIOR PELING DATE: 1999-11-12

PRIOR PELING DATE: 1999-11-12

PRIOR PLILING DATE: 2000-01-12

PRIOR PELING DATE: 2000-01-12

PRIOR PLILING DATE: 2000-01-13

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277 ValGluGluAsnValAlaAlaValThrGluLeuGluSerLeuGlyMetAspGlnGluThr 296
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                       914 CTGCGGATTAACTTGGACGCGATCTTCGAC----
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Best Local Similarity:
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DB:
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Matches:
Conservative:
Mismatches:
Indels:
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 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 7144
LENGTH: 3014
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ORGANISM: DROSOPHILA
US-11-097-143-7144
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Mismatches:
Indels:
                                    Clone ID: LIB3825-027-Q6-N6-G2
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| Sequence 7144, Application US/11097143
| Publication No. US2005020855841
| GENERAL INFORMATION:
| APPLICANT: Venter, J. Craig
| APPLICANT: et al.
| TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC
| TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC
| TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC
| TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC
| TITLE OF INVENTION: DETECTION KIT, SUCH AS NUC
| TITLE OF INVENTION: DETECTION RULES.
| FILE REPERENCE: CLOOD728
| CURRENT APPLICATION NUMBER: 60/157,832
| PRIOR APPLICATION NUMBER: 60/160,191
| PRIOR PILING DATE: 1999-10-28
| PRIOR PILING DATE: 1999-11-2
| PRIOR APPLICATION NUMBER: 60/161,932
| PRIOR PILING DATE: 1999-11-2
| PRIOR APPLICATION NUMBER: 60/164,769
| PRIOR PILING DATE: 1999-11-28
| PRIOR PILING DATE: 2000-01-12
| PRIOR PILING DATE: 2000-01-12
| PRIOR PILING DATE: 2000-01-12
| PRIOR PILING DATE: 2000-03-23
| NUMBER OF SEQ ID NOS: 43008
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ORGANISM: Gossypium hirsutum

PEATURE:

1 PEATURE:

1 OTHER INFORMATION: Clone ID:

US-10-021-323-3629
                                                                                                                                     Percent Similarity:
Best Local Similarity:
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US-11-097-143-7144/c
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1076 GATTAACCTGGACGCGATC-------TTCGACGGTCTCACTTCCCA 1038
                                       278 uGluagnValAlaalaValThrGluLeuGluSerLeuGlyMetaggGlnGluThrLeuSe 298
                                                                            298 rGluvalGlualaIleLeuGluProValLysAsnLeuThrTrpProSer 314
    8 6 8 6 8 6
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Search completed: November 13, 2005, 11:33:41 Job time : 917 secs

protein

Run on:

Sequence:

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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menzrd, M., Cruaud, C., Quetler, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: sequences are based on single pass reads.

Life Technologies (a division of invitrogen) members carried out

full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

MRGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis
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BX839165 Arabidopsis thaliana Adult vegetative tissue Col-0
Arabidopsis thaliana cDNA clone GSLTLS582B09 5PRIM, mRNA sequence.
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Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Fopermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
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-MODEL=frame+ p2n.model -DEV=xlh
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-UNTIS=bits -START=1 -END==1 -MATRIX-BLOORE=5 - ALIGNESOORE=5 - ALIGN
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CK253464 EST737101
CK251403 EST735040
                                                                                                                                                             November 13, 2005, 08:38:59; Search time 3686 Seconds (without alignments) 3294.222 Million cell updates/sec
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                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                       frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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CK24536
AY106400
CL979301
CK245431
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, Ygapext
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , Y
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                                                                                                                                                                                                                                                                  MetThrLyslleGluLeuArgAlaLeuGlyAsnThrGlyLeuLysValSerAlaValGly
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Matches:
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1367.00
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Best Local Similarity:
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CK253464 1953 bp mRNA linear EST 30-JUL-2004 EST737101 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCC562 5' end, mRNA sequence. CK253464
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Solanum tuberosum
Solanum tuberosum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.

1 (bases 1 to 953)
Solanales; Solanaceae; Solanum.

2 (bases 1 to 953)
Concart: Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Contact: Robin Buell
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-arrayaeigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                         /note="Wector: pCMVSport6.1; Site 1: EcoR1; Site 2: Not1; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
                                  813
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lAlaHisCysLysSerLysGlyLysLysIleThrLysLeuAlaLeuGlnTyrSerLeuAl
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                                                                                                                                                       US-10-606-300-11 (1-319) x CK253464
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Pred. No.:
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KEYWORDS
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ORGANISM
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DB:
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AUTHORS
TITLE
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/note="Vector: pCMVSport6.1; Site 1: EcoR1; Site 2: Not1; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
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                                                      Genomics
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/clone ltype="callus"
/clone ltype="pocato callus cDNA library, normalized full-length"
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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Solanum tuberosum
Eukaryota, Viridalinatae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Visidalinatae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
I (bases I to 998)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Other ESTs EST35041
Contact: Robin Buell
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     GAAGCCTTTCGCCTCGGCGTCAATTTCTTTGACACTTCCCCGTATTATGGAGGAACGTTA 189
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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E 1 (bases 1 to 947)

S Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTS from potato callus tissue

L Unpublished (2003)

Other ESTS: EST733785

Contact: Robin Buell

The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seg primer: ATT TRG GTG ACA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                               EST733784 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCEDB00 5' end, mRNA sequence. CK250147 CK50147.1 GI:39801934
                                                                                                                               283
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                                                           804
                                                                                 LysSerLysGlyLysLysIJeThrLysLeuAlaLeuGlnTyrSerLeuAlaAsnLysGlu 263
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/db_xref="taxon:4113"
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GTGGGGGTGATCAGTGCTTCTCTCTTTCAATGGGTCTTTTACTGAGGCTGGTGGTCGT
                                              264 IleSerSerValLeuValGlyMetSerSerValSerGlnValGluAsnValAlaAla
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Solanum tuberosum (potato)
Solanum tuberosum
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CK243867

EST737504 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCA594 5' end, mRNA sequence.
CK243867
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EST.
Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Core eudicots;
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831 283

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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMAD20"
/tissue_type="abiotic and biotic stress-treated leaves,
callus_tissue and root tissue"
/tissue_type="abiotic and biotic stress-treated leaves,
callus_tissue and root tissue"
/lab host="DH10B-TONA"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCWVSport6.1; Site 1: ECORI, Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
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Micotiana benthamiana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterida; lamilds; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 979)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
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                                       224 GluTrpHisProAlaSerProGluLeuLysSerAlaSerLysAlaAlaValAlaHisCys
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                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2003)
Other EST9: EST745256 EST745257
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Ariz
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualiflers
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asterids; lamiids; Solanales; Solanaceae; Solanum.

I (bases 1 to 948)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue

L Unpublished (2003)
Cother ESTs: EST727503
Contact: Robin Buell
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9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tlgr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pCMVSport6.1; Site 1: EcoR1; Site 2: Not1; supplier: RNA was isolated from Solanum tuberosum var. Kennebec callus tissue grown on solid media."
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full-length"
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Gaps:
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Spermatophyta, Magnoliophyta, Liliopaida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu, TICR,
www.tigr.org; or NCBI, www.ncbi.nlm.nin.gov. When the source of t
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 ATGGAGCTCCGCGAGCTGGGCGGTACGGGTCTCCGCGTCAGCGCCGTCGGCTTTGGTGCC
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Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V. Maize Mapping Project/DuPont Consensus Sequences for Design (Overgo Probes Unpublished (2002)
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Email: chenchengenomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

E 1 (bases 1 to 1302)

S Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao,M., Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis

L Unpublished (2004)
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OBIFCCO33028 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
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TGTAGAAAGAAGAGAAAAAGCATTACGAAGCTAGCTATGCAGTACAGCTTAATGAACAAT
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                        GTCGCCACCAAGTGCGGCCGCTACAAGACGAGGTTTCGACTTCTCCGCCAACCGTGTG
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Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
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CKZ57246
EST740883 potato callus CDNA library, normalized and full-length Solamum tuberosum cDNA clone POCD393 S' end, mRNA sequence. CKZ57246.1 GI:39814226
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.

(bases 1 to 936)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Other_ESTs: EST740884
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                                                                                                                                                                                                                                                                                                                                                       Solanum tuberosum (potato)
Solanum tuberosum (potato)
Solanum tuberosum
Solanum tuberosum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Subarids; lamids; Solanales; Solanaceae; Solanum.

E 1 (bases 1 to 945)
Subarids; Solanales; Solanaceae; Solanum.

Generation of ESTS from potato callus tissue
L Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Emall: potato-arrayetigr.or
Small: potato-arrayetigr.or
Ilocato-arrayetigr.or
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                          CK245431

945 bp mRNA linear EST 30-JUL-2004
EST729068 potato callus cDNA library, normalized and full-length
Solamum tuberosum cDNA clone POCAE26 5' end, mRNA sequence.
CK245431.1 GI:39791983
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    AAGAAGAAGAGAAAAACATTACAAAGCTAGCTATGCAGTACAGCTTGATGAACAATGAG
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supplier: RNA was isolated from Nicotiana benthamiana
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grown plants, heat-stressed leaves (5 C 3 hr, 6hr), and pathogen
cold-stressed leaves (Fseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
                                                                                                                                                                                                                                                                                                                 CK286730 883 bp mRNA linear EST 02-AUG-2004 EST749452 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMB419 5' end, mRNA sequence.
                                                                                         244 LygSerLygGlyLygLygIleThrLygLeuAlaLeuGlnTyrSerLeuAlaAsnLygGlu 263
                                                                                                                                                                818 ÀÀÀGGAÀÀGGAÀAAGGAAATTCTCAAAATTAGCCTTGCAGTACCAGCTTAGCAATACCGAT 877
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                                    698 Grececerchicacricricricritrical desircritria creasecrecrecreca
                                                                      224 GluTrpHisProAlaSerProGluLeuLysSerAlaSerLysAlaAlaValAlaHisCys
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Matches:
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Mismatches:
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'\note="Vector: pCMVSport6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 ValAlaThrLysCysGlyArgTyrLysGluGlyPheAspPheSerAlaGluArgValArg 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338 GTGTCTACAAAATGTGGGAGGTACAAAGAGGGATTTGATTTTAGTGCTGAGAGAGTGACT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisAspileGluPheGlySerLeuAspGlnIleValSerGluThrIleProAlaLeuGln 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerGluLygMetLeuGlyLygGlyLeuLygAlaLeuGlnValProArgSerAgpTyrIle 83
                                                                                                                                                                                                                                        /tissue_type="callus"
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                                                                          Arizona Genomics
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Ar
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:

    .936
    /organism="Solanum tuberosum"

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82.44%
73.44%
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/tissue_Type="abjoit and biotic stress-treated leaves, tissue_type="abjoit and biotic stress-treated leaves, callus tissue and root tissue"

/lab host="DH10B-TonA"
/clone_lib="Micotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
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supplier: RNA was isolated from Nicotiana benthamiana tissues that include callus, roots from liquid culture grown plants, heat-stressed leaves (5 C 3 hr, 6hr), and pathogen cold-stressed leaves (5 C 3 hr, 6hr), and pathogen challenged leaves (Feeudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr, and Kanthomonas campestris pv campestris la hr, 18hr; mandestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."
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                                                                                                                                                                                      of Arizona Genomics
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               1 (bases 1 to 922)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
Greeration of EST sequences from Nicotiana benthamiana Unpublished (2003)
Contact: Robin Buell
asterids; lamiids; Solanales; Solanaceae; Nicotiana
                                                                                                                                                               Email: potato-array@tigr.org
Clones can be requested from the University of Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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222
16
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                                                                                                                              The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850,
                                                                                                                                                                                                                                                           1. .922
/organism="Nicotiana benthamiana"
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Matches:
Conservative:
Mismatches:
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Pred. No.:
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EST747208 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMA037 5'
end, mRNA sequence.
CK284486.
CK284486.1 GI:39858105
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Nicotiana benthamiana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
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                                                                                                                                              SerProLeuGlySerValPheGlyProValAlaGluAspAspAlaValAlaThrValArg
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83

Challenged leaves (Pseudomonas syringae pv tomato 12 hr; Xanthomonas campestris pv campestris 12 hr, 18hr; Pseudomonas syringae pv phaseolicola 18hr; and Xanthomonas campestris pv vesicatoria 18hr). RNA was isolated from these tissues and pooled in approximately equal molar amounts."  Alignment Scores: Pred. No.: 1.84e-112	4 IleGluLeuarghlaLeudlyAsnThrdlyLeuLysvalSeralavalGlyPheGlyAla	4 GINALPHARYGUEGITHERNING	CK282535/c LOCUS CK282535 926 bp mRNA linear EST 02-AUG-2004
Db 475 CATGATATTGAGTTTGGGTCTCTTGATGGAATGTGAATGAGACGCTTCCAGCCCTTCAG 534  Qy 144 LysLeuLysGlnGluGlyLysThrArgPheIleGlyIleThrGlyLeuProLeuAspIle 163  Db 535 AAACTGAAGCAGGTGGAAAGATCGTTTCATTGGTATAACCGGCCTTCCATTGGGATA 594  Qy 164 PheThrTyrValLeuAspArgValProProGlyThrValAspValIleLeuSerTyrCys 183  Db 595 TTCACTTATTGTGCTTGATCGGTACCTCGGAACGATTGATT	224 775 244 835	POY 264 ILESENSENTALIGUATED WENT 11	grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr), cold-stressed leaves (5 C 3 hr, 6hr), and pathogen

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supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (5 C 3 hr, 6hr), and pathogen
challenged syringae pv campestris 12 hr, 18hr;
Ranthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
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Nicotiana Denthamiana
Nicotiana Denthamiana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Nicotiana

12. (bases 1 to 926)
13. Staskawicz, B., Jin,H. and Baker, B.
Staskawicz, B., Jin,H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana

14. Unpublished (2003)
15. Other ESTS: EST745256 EST745259
16. Contact: Robin Buell
17. The Institute for Genomic Research
17. Medical Center Dr. Rockville, MD 20850, USA
17. Medical Center Dr. Rockville, MD 20850, USA
17. Medical Center Dr. Rockville, MD 20850, USA
17. Medical Center Dr. Rockville, MD 20850, USA
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17. Medical Ce
EST745257 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBWAD20 3'
end, mRNA sequence.
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SM Nicotiana Denthamiana

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; lamiids; Solanales; Solanacea; Nicotiana.

1. (bases 1 to 859)

Staskawicz, B., Jin, H. and Baker, B.

Generation of EST sequences from Nicotiana benthamiana

Unpublished (2003)

Contact: Robin Buell

The Institute for denomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.or

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACTA TAG.
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BST760349 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMDA27 5'
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Length:
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Conservative:
Mismatches:
Indels:
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859 206 114 0

US-10-606-300-11 (1-319) x CK297635 (1-859)

297 357 ValAlaThrLysCysGlyArgTyrLysGluGlyPheAspPheSerAlaGluArgValArg 103 123 477 HisAspileGluPheGlySerLeuAspGlnIleValSerGluThrIleProAlaLeuGln 143 537 597 PheThrTyrValLeuAspArgValProProGlyThrValAspValIleLeuSerTyrCys 183 HisTyrGlyValAsnAspSerThrLeuLeuAspLeuLeuProTyrLeuLysSerLysGly 203 717 ValGlyVallleSerAlaSerProLeuAlaMetGlyLeuLeuThrGluGlnGlyProPro 223 777 177 237 LysLeuLysGlnGluGlyLysThrArgPheileGlyIleThrGlyLeuProLeuAspile 163 657 43 83 63 SerProLeuGlySerValPheGlyProValAlaGluAspAspAlaValAlaThrValArg TIGCAGCTCCGACCACTGGGCAACACCGGCCTCAACCTTAGCTCCGTCGGCTTCGGCGCT TCTCCTCTTGGCAAAGTCTTCGGCGATGTCTCCGAACAAGACGCCTTCGCCGCCGTGCGC SerGluLysMetLeuGlyLysGlyLeuLysAlaLeuGlnValProArgSerAspTyrIle 298 TCAGAAAAGGTACTAGGAAAGGCTTTGAAGGCTCTTGGAGGCTCCTAGAGATGATT TICACTTATGTGCTTGATCGGGTACCTCCAGGAACGGTTGATGTTATTCTGTCATATTGT CACTACAGTATCAATGACTCAACTTTGGAGGATCCGTTGCCATACCTGAAGAGAGCAAGGGT GTGGGAGTGATCAGTGCTTCCCTCTTGCAATGGGTCTTCTTACTGAGGCTGGAGCTCCA 4 IleGluLeuArgAlaLeuGlyAsnThrGlyLeuLysValSerAlaValGlyPheGlyAla 24 178 44 238 64 84 358 104 418 124 478 144 538 164 298 184 204 ઠે 셤 ò ઠ 셤 ઠ a ò a ò 셤 ઠે 요 ò 요 ò 셤 ò 유 à 셤

224 GluTrpHisProAlaSerProGluLeuLysSerAlaSerLysAlaAlaValAlaHisCys 243

248 AAAGGAAAGGGAAAG 852 244 LysSerLysGlyLys 838 셤 g ઠે

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Result No.	Score	Ouery Match	Query Match Length	DB	ID	Description
	1619	100.0	319	4	AAE11998	Aae11998 Arabidop
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7	420.5	26.0	294	4	ABB60118	Abb60118 Drosophi
œ	366	22.6	329	~	AAR51284	Aar51284 L-fucose
თ	339.5	21.0	321	7	AAR27118	
10	337.5	20.8	306	œ	ADS44757	Ads44757 Bacteria
11	329.5	20.4	304	9	ABU17641	Abul7641 Protein
12	327	20.2	325	œ	ADN22222	Adn22222 Bacteria
13	322	19.9	308	œ	ADN24982	Adn24982 Bacteria
14	322	19.9	329	9	ABU29907	Abu29907 Protein
15	317	19.6	367	7	ABO77872	Abo77872 Pseudomo
16	316	19.5	307	œ	ADS27427	Ads27427 Bacteria
17	316	19.5	346	9	ABU27806	Abu27806 Protein
18	314	19.4	325	ß	ABP65908	Abp65908 Bifidoba
19	313	19.3	326	4	AAU34593	
20	313	19.3	326	9	ABU15320	Abul5320 Protein
21	313	19.3	326	œ	ADN18209	Adn18209 Bacteria
22	311	19.2	346	Ŋ	AAM4 9053	Aam49053 Coriolus
23	310.5	19.2	302	9	ABU43680	Abu43680 Protein
24	310	19.1	311	9	ABU17621	Abul7621 Protein
52	307.5	19.0	311	œ	ADS30346	Ads30346 Bacteria

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Abu47024 Protein e	Aau36253 Pseudomon	Abu47649 Protein e	Abo81330 Pseudomon	Abul7897 Protein e	Ads41735 Bacterial	Ads30364 Bacterial	Abu30072 Protein e	_	Ada34792 Acinetoba	Ads23006 Bacterial	Ads41580 Bacterial	Ads24931 Bacterial	Abul6921 Protein e	Abu42693 Protein e	Abp38281 Staphyloc	Ads04717 Staphyloc	Abu34174 Protein e	Aay52837 Escherich	Aau34474 E. coli c
ABU47024	AAU36253	ABU47649	ABO81330	ABU17897	ADS41735	ADS30364	ABU30072	ADC97264	ADA34792	ADS23006	ADS41580	ADS24931	ABU16921	ABU42693	ABP38281	ADS04717	ABU34174	AAY52837	AAU34474
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306.5	305.5	305.5	302.5	302	301.5	300.5	296.5	296.5	296	295	294.5	294.5	294	291.5	291.5	291.5	291	291	291
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1

The present invention relates to an isolated protein having L-galactose dehydrogenase (L-galDH) biological activity. L-galDH uncleic acid is useful for generating transgenic organisms and modified pants with enhanced ability to synthesise ascorbic acid. L-galDH facilitate the production of a plant that has been genetically modified to express a mutated L-galDH protein which is resistant to herbicides that act against the naturally occurring L-galDH and to identify and/or design compounds that are inhibitors of L-galDH and to identify and/or design compounds the enzyme. The present sequence is Arabidopsis thalls plants that express the enzyme. The present sequence is Arabidopsis thalian L-galactose dehydrogenase (L-galDH) protein. The L-galDH gene is located on L-galactose dehydrogenase; L-galDH; transgenic organism; ascorbic acid; herbicide; chromosome 4. Novel L-galactose dehydrogenase protein and nucleic acid sequence encoding the protein for producing genetically modified plants and microorganisms with enhanced ability to synthesize ascorbic acid. Arabidopsis thaliana L-galactose dehydrogenase (L-galDH) protein. Claim 1; Page 57-58; 58pp; English. AAE11998 standard; protein; 319 AA. 29-MAR-2001; 2001WO-GB001412. 29-MAR-2000; 2000GB-00007651. (first entry) Smirnoff N, Wheeler G; Arabidopsis thaliana. (ASCO-) ASCORBEX LTD. WPI; 2001-616482/71. N-PSDB; AAD19526. WO200172974-A2. chromosome 4 18-DEC-2001 04-OCT-2001 AAE11998; 

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precursor into ascorbic acid, culturing the recombinant yeast in a medium comprising an ascorbic acid precursor, thus forming ascorbic acid, and isolating the ascorbic acid. Also include are stabilishing ascorbic acid acid or its salt and a recombinant yeast in a medium comprising cascorbic acid or its salt and a recombinant yeast functionally cascorbic acid or its salt and a recombinant yeast functionally cartivity selected from L-galactose dehydrogenase (LGDH), L-galactono-1, 4-lactone dehydrogenase (AED), D-arabinose dehydrogenase (AEA), D-capinono-1,4-lactone oxidase (GLO) arabinono-1,4-lactone oxidase (ALO), L-gulono-1,4-lactone oxidase (GLO) carabinone dehydrogenase (AEA), D-capinono-1,4-lactone oxidase (GLO) cor is capable of producing at least about 25% ascorbic acid precursor of converting to ascorbic acid at least about 25% ascorbic acid precursor cor is capable of producing at least about 25% ascorbic acid precursor. The ascorbic acid produced (Vitamin C) is a powerful antioxidant, a deficiency of which causes scurvy in humans. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generating ascorbic acid or its salt, involves culturing yeast capable converting ascorbic acid precursor into ascorbic acid in medium comprising ascorbic acid precursor, and isolating ascorbic acid.
                                                                                                                                                                                                                                       LHCHDIEFGSLDQIVSETIPALQXLKQEGKTRFIGITGLPLDIPTYVLDRVPPGTVDVIL
                                                                                                                                                                                                                                                                                                                    181 SYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAAV
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                                                    Length 319;
                                                   ; Score 1619; DB 4;
; Pred. No. 2.7e-141;
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 termination sequence
                Arabidopsis thaliana
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05-MAR-1999;
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16-APR-1999;
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                                                                                                                                                                                                                                                                                   8 ALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEKM
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99US-0158029P.
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99US-0158234P.
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Best Local Similarity 99.7
Matches 311; Conservative
               12-071-1999
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Length 253;
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Best Local Similarity 100.0%; Pred. No. 1.4e-110;
Matches 253; Conservative 0; Mismatches 0;
9905-0153070P

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9905-0155486P

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 VILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidaring cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175 and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KASEVCKERGVELGKLAMYYTMSGLPEVSTFLTGMQTRQLLRINLDA-NEVGLSDKEQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 AAVAHCKSKGKKITKLALQYSLAN-KEISSVLVGMSSVSQVEENVAAVTELESLGMDQET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
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                                                                                                      developmental biology; cell signalling; insecticide;
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                                                                          Drosophila melanogaster polypeptide SEQ ID NO 28023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 Match 36.7%; Score 593.5; DB 4; Local Similarity 42.5%; Pred. No. 3.6e-46; ne 128; Conservative 63; Mismatches 99;
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                                                                                                                                                                                                                                                                                                                                                Myers
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                                    Drosophila melanogaster
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                                                                                                                   pharmaceutical
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81 GKSEELLGQALK--DVPREAYYIATKVARYELDPINMFDYTAAKARESVKRSLELLQLDR 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isolated nucleic acid detection reagent for detecting 1000 or more se from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 40479.
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ABB71229 standard; protein; 342
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Matches 117; Conservative
                                                                                                                                                                                                                                                                                                Drosophila melanogaster.
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                                                                                                                                                                                                                                           pharmaceutical
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                                                                                                          26-MAR-2002
                                                                                                                                                                                                                  Drosophila;
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111 DILQVHDVDAAPNLDIVLNETIPVLEEYVQAGKARFIGVTAYDVDVLKECAER-GKGRIQ 169
                                                                                                                                     230 RGARICQQRNVELGKLAMYYTWQLDGAATFLIGIPNRKLLRINLDAIFD----GLTSHEQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || |: ::|:| | ::|| || 67 LGAFLQT--KPRDEFV9JTKAGRLLRPNPERRPSGLDTDNDFHVPDDLRREWDFTEQGIR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 ASIAESQERIGLDRIDLLYLHDPERHDLDLALASAFPALEKVRAEGVVKAIGIGSMVSDA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 LTRA---VREADLDLIMVAGRY----TLLEQPAATEVLPACAENATGIVAASVFNSGLL 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 new recombinant DNA and the prepn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The L-FDH gene is new and can be used for the recombinant prodn. of the enzyme. (Updated on 16-OCT-2003 to standardise OS field)
                                                        104 KSIDESLERLQLDYVDILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDI
                                    178 VILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEGGPPEWHPASPELKSASK
                                                                                                                 238 AAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGM---DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGKGLKALQVPRSDYIVATKCGR-------YKEGFDFSAERVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTYVLDRVPPGTVDVILSYCHYGVNDSTLL-----DLLPYLKSKGVGVISASPLAMGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 ALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.6%; Score 366; DB 2; Length 329;
3est Local Similarity 30.7%; Pred. No. 4.2e-25;
4atches 103; Conservative 62; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KIKK ) KIKKOMAN CORP.
(NODA ) ZH NODA SANGYO KAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel L-fucose dehydrogenase gene - a of L-FDH using a L-FDH vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-fucose dehydrogenase; L-FDH; enzyme
                                                                                                                                                                                                                                                                                                                                AAR51284 standard; protein; 329 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas sp; No.1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-fucose dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                               (revised)
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N-PSDB; AAQ62089.
                                                                                                                                                                                            ETL 297
                                                                                                                                                                                                                                EVL 288
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14-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 DILHCHDIEFG-SLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVD 177
  KAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGMDQET 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                          KRGAEICQKRNVELGKLAMYYTMQLDGAATFLIGIPNRKLLRINLDAIPD----GLTSHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----FPDDYDREEGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LSEKMLGKGLKALQVPRSDYIVATKCGRY----KEGFDFSABRVRKSIDESLERLQLDYV
                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 7146; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster polypeptide SEQ ID NO 7146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 RMEYRQLGSTGLHVSKLAIGGSPLCNL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.0%; Score 420.5; DB 4; 33.7%; Pred. No. 3.2e-30;
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                                                                                                                                                                                                                ABB60118 standard; protein; 294 AA
                                                                             297 LSEVEAILEPV--KNLTWPS 314
                                                                                                   SEVLQYLRENVFTKSYSWGS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PWD,
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                                                                                                                                                                                                                                                                                         (first entry)
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Best Local Similarity 33.77
Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster.
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N-PSDB; ABL04221.
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                                                                                                                                                                                                                                                                                                                                                                                         pharmaceutical
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                                                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                        Drosophila;
  237
                                        258
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                   234 RPAANATYNYAPAPQELLDRANLADVCESHGTTLPAAALHFPYQHPAVTSVVLGMRTPA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transforming a plant where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                         ERLOLDYVDILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGI----TGLPLDIFTY
                                                                             167 VLDRVPPGTVDVILSYCHYGVNDSTLL-----DLLPYLKSKGVGVISASPLAMGLLTEQ
                                                                                                                                                            221 GPP-----EWHPASPELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 23187; 122pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen X,
                                                                                                                                                                                                                                                                                                                                                                                             ADS44757 standard; protein; 306 AA
                                                                                                                                                                                                                                                                     294 QVKQNLDLASQTVPDQLWAD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Slater SC,
                                                                                                                                                                                                                                                276 QVEEN--VAAVTELESLGMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacterial polypeptide #23187.
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SLATER S C.
CHEN X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-061375/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003233675-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ADS44757;
                                                                                                                     185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria.
111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKALOVPRSDYIVATKCGRY-----KEGF-----DFSAERVRKSIDESL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic DNA from Arthrobacter oxidans F1 was subjected to restriction enzyme analysis and the N-terminal amino acid sequence of L-fucose dehydrogenase determined. A degenerate probe was synthesised based on this amino acid sequence. The probe was used to screen an Arthrobacter CDNA library to isolate a L-fucose dehydro- genase clone. The isolation of such a clone provides a convenient method for prodn. of L-fucose dehydrogenase without the need for induction by L-fucose. The probe may be used to evaluate the extent of expression of L-fucose dehydrogenase. The DNA sequence is widely used to assay L-fucose levels. The protein equence of L-fucose dehydrogenase may be used to produce antibodies. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 TGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSBKMLGKG
                                          늉
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated gene encoding L-fucose dehydrogenase - useful for prodn.
enzyme by genetic engineering.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.0%; Score 339.5; DB 2;
ilarity 30.9%; Pred. No. 1.2e-22;
Conservative 58; Mismatches 110;
                                                                                                                            297 RPAQLIQNAEYAALEIPA-GLWAE-LAEARLIPTP 329
                                                                                                    273 SVSQVEENVA-AVTELESLGMDQETLSEVEAILEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arthrobacter oxidans; F1; induction; assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kato I;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 8; 16pp; English.
                                                                                                                                                                                                                                                AAR27118 standard; protein; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sakai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92EP-00302170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91JP-00089184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TAKI ) TAKARA SHUZO CO LTD.
                                                                                                                                                                                                                                                                                                                               (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arthrobacter oxydans; Fl.
                                                                                                                                                                                                                                                                                                                                                                                                                  Fucose dehydrogenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1992-325548/40.
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Matches 99; Conserv
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tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomanan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                    67 MLGKGLKALQVPRSDYIVATKCG-RYKEG-----FDFSAERVRKSIDESLERLQLDYVDI 120
                                                                                                                                                                                                                                                                                                                                                                                                     121 LHCHDIBFGSLDQIVSETIPALQKLKQEGKTRFIGITGL-PLDIFTYVLDRVPPGTVDVI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 -PELKSASKA--AVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAA--- 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                        SIMMQFSLFDRRPEEWLPLLEEHQISVVARGPVAKGLLTEK-PLDQASESMKQNGYLSYS
                                                                                                                                                                                                                                                                                                                     7 RALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEK
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                                                                                                                                                                                                                                                                                        Gapa
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                                                                                                                                                                                                                                                       Length 306;
                                                                                                                                                                                                                                                                                    64; Mismatches 108; Indels
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                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                    20.8%; Score 337.5; DB 8 31.3%; Pred. No. 1.7e-22;
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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Matches 100; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                       Sequence 306 AA;
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25-OCT-2001;
08-FEB-2002;
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Syskind JW;

Malone C, Haselbeck R, Ohlsen KL,

Zamudio C,

Wang L,

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid object acid inhibites proliferation of sinhibited by the antisense nucleic acid, (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the nucleic acid; (4) an antibody capable of specifically binding the polypeptide or that has an activity of agene in an operor required for proliferation or that plants polypeptide; (6) inhibiting cellular proliferation or that inhibits cellular proliferation or that biological pathway required for proliferation, (7) identifying a compound that inhibits proliferation; (8) identifying a gene required for cellular proliferation or that biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acis; (9) manufacturing an antiblocit; (10) profiling a compound a activity; (11) a culture comprising strains in which the gene or product is overexpressed or underexpressed; (12) determining the extent to which each of the strains of strains; or (13) identifying the extent in a culture or collection of strains; or (13) identifying the extenting for homologous nucleic acids are useful for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. acruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at Everypent Sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
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                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LHCHDIEFGSLDQIVSETIPALQKLKQEGKTRPIGITGLPLDIFTYVLDRVPPGTVDVIL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKAAVAHCKSKG-----KKITKLALQYSLANKBISSVLVGMSSVSQVEENVAAV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 DYLSYSYDELYĞTLANVKELIVESSLTGTALQYCLHNDTVAAVIPGASSIQQLRENVQAC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 RALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPXYGGTLSEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RQLGNSDLFVTEMGLGCMSLGT----SEAEAMRIIDEAIDLGINFFDTADLYDYGLNEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SYCHYGVNDSTLL----DLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSA
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Xu HH
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Porsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.4%; Score 329.5; DB 6; 30.3%; Pred. No. 9.1e-22; iive 56; Mismatches 109;
Yamamoto R,
                                                                                                                                                                                                   Claim 25; SEQ ID NO 45565; 1766pp; English.
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 30.3%
watches 92; Conservative
Trawick JD,
                                            WPI; 2003-029926/02
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Pred. No. 1.7e-21;

27.68;

Best Local Similarity

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant baving an improved property. The plant is a crop plant such as maize or soybean. The method of producing a plant with the cerembinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant with the cerembinant DNA construct is useful for improving plants with the polynucleotide or polypeptide is useful for producing plants with the recombinant DNA construct is useful for improving plants with concreased resistance to plant disease, better growth rate by modification of the concent, improved yield by modification of carbohydrate, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of phosphorus use and/or uptake, by modification of phosphorus use and/or uptake, by modification of protein yield and/or content, improved lighin production or improved galactomannan condition, improved lighin production or improved galactomannan production. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a promoter positioned to provide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                                                                                                                                                 cold tolerance, heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
                                                                                                                                                                                                   Recombinant DNA construct; transformed plant; improved plant property;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldman BS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 4875; 122pp; English.
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                                     ADN22222 standard; protein; 325 AA.
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                                                                                                                                                           Bacterial polypeptide #4875.
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HINKLE G J.
SLATER S C.
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                                                                             ADN22222;
                                                                                                                                                                                                                                                                                                                                                              Bacteria.
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(SLAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAOY/)
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RESULT 12
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                                                                                                                                                                                                           : ||:||:||::||::|| || 62 --WYPRDQYVLSTKVGRLLKPRRABIDFAPWVDGLPFEPVFDYSYDGTMRSIEDSLQRL
                                                                                                                                                                                                                                                                                                                       ----YKEGFDFSAERVRKSIDESLERL
                                                                                                                                                                                                                                                                                         114 QLDYVDILHCHDIEFGS-----LDQIVSETIPALOKLKQEGKTRFIGITGLPLDIFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             177 VAHEAIRRODFDCLLLAGRYTLLEQDALDGFLPLCEKKQVSVILGGGYNSGILATGAVPG
                                                     14 LKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEKMLGKGLK
                                                                                                                                                                                                                                                                                                                                                                                                       166 YVLDRVPPGTVDVILSYCHYGVNDSTLLD-LLPYLKSKGVGVISASPLAMGLLTEQGPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- EWHPASPELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEEN
Gaps
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Mismatches 114;
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                                                                                                                                                                       74 ALQVPRSDYIVATKCGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADN24982 standard; protein; 308 AA.
199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-FEB-2002; 2002US-0360039P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial polypeptide #7635.
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  Conservative
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SLATER S C.
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297 L 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-2004
        83;
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Matches
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promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant the recombinant DNA construct and are method of producing a transformed plant the swing an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant, where the copymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance. The recombinant DNA construct is useful for producing plants with construct is useful for producing plant such the cold increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or of the cold or uptake, by modification of exbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactemannan production. This sequence represents a bacterial polypeptide used in the scope of the printed specification but was obtained in electronic formant of the printed specification but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            format from USPTO at segdata.uspto.gov/sequence.html
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Sequence 308 AA;

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77 VPRSDYIVATKCGR-------YKEGFDFSAERVRKSIDESLERLOLD 116
                                                                                                                                                   YYDILHCHDIEFGS-----LDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVL 168
                                                                                                                                                                                                                 DRVPPGTVDVILSYCHYGVNDSTLLD-LLPYLKSKGVGVISASPLAMGLLTEQGPP---- 223
                                                                                                                                                                                                                                                                                           EAIRRODFDCLLLAGRYTLLEQDALDGFLPLCEKKQVSVILGGGYNSGILATGAVPGAKY 235
                                                                                   224 EWHPASPELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENV 281
                                                                 17 SAVGFGASPLGSVFGPVAEDDAVATVREAFRIGINFFDTSPYYGGTLSEKMLGKGLKALQ
ch 19.9%; Score 322; DB 8; Length 308;
1 Similarity 27.5%; Pred. No. 4.6e-21;
82; Conservative 65; Mismatches 113; Indels 38; Gaps
                                                                                                                                                                                                                                                                                              176
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Best Local
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Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                  Protein encoded by Prokaryotic essential gene #15434.
                ABU29907 standard; protein; 329 AA
                                                                                                                                                     21-MAR-2002; 2002WO-US009107
                                                  (first entry)
                                                                                                   Enterococcus faecium.
                                                                                                                    WO200277183-A2
                                                  19-JUN-2003
                                  ABU29907
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AS------PELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGM 271

228

2001US-00815242. 2001US-00948993.

21-MAR-2001; 06-SEP-2001;

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid containing the vector; (3) an isolated encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation, or that an ancivity against a bloological pathway required for proliferation, or that that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the bloological pathway required for proliferation or that that inhibits proliferation of an oraquired for cellular proliferation of an oraquired for cellular proliferation of an oraquired for cellular proliferation of an organism acts; (9) manufacturing an antibloicic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or obliferation of an organism. The antisense nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational drug discovery programs, or for screening for homologous nucleic acids required for proliferation to isolate candidate molecules for rational corrupt form part of the printed specification, but was obtained in heterronic format directly from WiPo at the sequences
                                                                                                                                                                                                                                                          New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 --LSEKMIGKGLKA-LQVPRSDYIVATKCGRYKEGFDFSAERVRKSI----DESLERLQL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYVDILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGIT---GLPLDIFTYVLDRVP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 PGTVDVILSYCHYGVNDSTLL--DLLPYLKSKGVGVISASPLAMGLLTEQ---GPPEWHP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 KMEYRKSGHSGLKLPILSLGLWONFGDYDPIHNOREI--LRGAFDMGITHFDLANNYGGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                         Zyskind JW;
Xu HH;
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Best Local Similarity 31.1%; Pred. No. 5e-21;
Matches 104; Conservative 60; Mismatches 124; Indels
                                                                                                                         Ohlsen KL,
Forsyth RA,
                                                                                                                            Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 57831; 1766pp; English.
                                                                                                                            Malone C,
Carr GJ,
                                       06-MAR-2002; 2002US-0362699P.
                                                                                     (ELIT-) ELITRA PHARM INC.
                                                                                                                            Zamudio C,
Trawick JD,
                                                                                                                                                                                              WPI; 2003-029926/02.
                                                                                                                                                                                                                     N-PSDB; ACA33777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and plarage in herapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial drugs, including anti-P. aeruginosa drugs, as templates for accombinant production of P. aeruginosa-derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-16 RBO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed sequence. The sequence of the printed sequence. The sequence of the printed sequence.
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243 AHRKEIPFLSEEQVGSTLEKIKALQTIAV----SRGQSLAQMALAWNLRQKSVTSVLVGA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           th 19.6%; Score 317; DB 7; Length 367; Similarity 29.3%; Pred. No. 1.7e-20; 84; Conservative 60; Mismatches 103; Indels 40; Gaps
                                                                                                                                                                                                                                                                                                     Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
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                                                  272 SSVSQVEENVAAVTELESLGMDQETLSEVEAILE 305
                                                                     | :||::|:| : |||
299 SRLSQLQESVRM---MDNLDFSPEEELRIDQILE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 26618; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Deloughery C,
                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa polypeptide #10047.
                                                                                                                                                                   AB077872 standard; protein; 367 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0074788P.
98US-0094190P.
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                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa
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N-PSDB; ABD11443.
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                                                                                                                                                                                                                                                                                                                                                                      US6551795-B1
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27-JUL-1998;
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Query Match
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US-09-630-983A-11

Sequence 11, Application US/09630983A

Patent No. 6630330

GENERAL INFORMATION:

APPLICANT: Bouer, Michael

TITLE OF INVENITON: AScorbic Acid Production from Yeast

TITLE OF INVENITON: 2028.594000

CURRENT APPLICATION NUMBER: US/09/630,983A

CURRENT FILING DATE: 2000-08-02

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

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RESULT 2 US-09-252-991A-26618

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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AEUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: AEUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENVAAVTELESLGMDQETLSEVEAIL 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 EISSVLVGMSSVSQVEENVAAVT 285
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Matches 94; Conserv
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US-09-252-991A-30076
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US-09-252-991A-30076
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Sequence 26618, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TYPLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERGEINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGEINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26618
LENGTH: 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 PPGTVDVILSYCHYGV--NDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPAS 229
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GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Stater, Steven C.
TITLE OF INVENTION: Wascaccus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-101584918
CURRENT APPLICATION NUMBER: US/09/902,540
FILE REPLACATION NUMBER: US/09/902,540
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 IELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.6%; Score 317; DB 4; Length 36
29.3%; Pred. No. 1.3e-24;
tive 60; Mismatches 103; Indels
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 29.34
Matches 84; Conservative
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SEQ ID NO 10503
LENGTH: 347
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Matches 87; Conservative
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280 NVAAVTELESLGMDQETLSE 299
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                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 332 amino acids TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 6891:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 LSEKWIGKGLKALQVPRSDYIVATK----CGRYKEGFDFSAERVRKSIDESLERLQLDYV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 ----VDVILSYCHYGVNDSTL-LDLLPYLKSKGVGVISASPLAMGLLT-----EQGPPEW 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 RELRVPFISNOPQYSMLYRVIEPQVIPASDEAGLGQIVWSPIAQGVLTGKYLPGQAPPAG 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---SPELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGM 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HERKLGRSGLVVSEISYGNWITHGS---QVEEEAALACVRAALDVGITTFDTADVYAAT 57
                                                      Patent No. 683347
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: However, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: However, Gregory J.
APPLICANT: Hinkle, Gre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 IELRALGNTGLKVSAVGFGA-SPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.6%; Score 300.5; DB 4; 29.0%; Pred. No. 6e-23;
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                Sequence 10805, Application US/09902540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97; Conservative
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Best Local Similarity
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US-09-902-540-10805
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Sequence 6079, Application US/09328352

Batent No. 6562958

GENERAL INFORMATION:
APPLICANT GATY L. Breton et al.
APPLICANT GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GT-99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
ERNGTH: 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 ILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVDVI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 ---LSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLT------BOGPPEWHP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 EDKYSLIHRQAEK----ELPPYLEKNKISFVPYPPLASGLLTGKYELGEEKQFGEGDPRK 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 ASPELKSASKAAVAHCKSKGKKITK-----LALQYSLANKEISSVLVGMSSVSQVEE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 RNPDFQGERFREILTAVDVLRPIAKRYQATPAQLVLAWYMKNPRVSVVIPGAKRPEQVSD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 BIR-IGHSQVYAEQLGLGANAVGGHNLFDGLEBDETGKQVVRTALNSGINLIDTAXAYGNG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 BLRALGNTGLKVSAVGFGASPLG--SVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
18.3%; Score 296.5; DB 4; Length 332;
Best Local Similarity 27.5%; Pred. No. 1.6e-22;
Matches 88; Conservative 63; Mismatches 132; Indels 37;
APPLICATION NUMBER: US/09/107,532A FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...332
SEQUENCE DESCRIPTION: SEQ ID NO: 6891:
                                                                                                                                                                                                                                                                 NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                 APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
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y APPLICANT: MIYAKE, Koichiro; HASHIMOTO, Shinichi; MOTOYAWA Hiroaki; APPLICANT: MIYAKE, Koichiro; HASHIMOTO, Shinichi; MOTOYAWA Hiroaki; APPLICANT: OZAKI, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji; TITLE OF INVENTION: A process for producing isoprenoid compounds by TITLE OF INVENTION: microorganisms and a method for screening compounds with; TITLE OF INVENTION: antibiotic or weeding activity

FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/673,198

CURRENT PILING DATE: 1998-04-14

PRIOR APPLICATION NUMBER: JP98/103101

PRIOR APPLICATION NUMBER: JP98/221910

PRIOR PILING DATE: 1998-08-05

PRIOR FILING DATE: 1998-08-05

PRIOR FILING DATE: 1999-02-15

NUMBER OF SEQ ID NOS: 34

SOPTWARE: PATENTIN Ver. 2.0
186 LIDNRPESLINDVHDKQVKILARGPVFKGLLTSKSVDVIDEKFKNGVLDY--TQDELGS- 242
                                                                                                                          243 ---TIASIKELESNITALSFKYLTSHDAMGSIIVGASSVEQLEENVR--NYYKEISLDQ- 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
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                                                                                 236 SKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGMDQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 348;
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US-09-489-039A-12541
; Sequence 12541, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09673198
Patent No. 6806076
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----IKSARNRVKDIEY 309
                                                                                                                                                                                                                                    296 TLSEVEAILEPVKNLTW 312
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Best Local Similarity
Matches 94; Conserv
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US-09-673-198-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERLOLDYVDILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175 HPIAAVQ-----HEYSLLTREFEQTHLQTIRELGISLVPYSPLSRGLIINTLDVN 224
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                                                                                                                                                          18.3%; Score 296; DB 4; Length 334; 27.0%; Pred. No. 1.8e-22; ive 62; Mismatches 128; Indels
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larity 27.1%; Pred. No. 4.9e-22;
Conservative 72; Mismatches 116;
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                                            ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                               Best Local Similarity 27.0 Matches 93; Conservative
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Best Local Similarity
Matches 86; Conserv
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US-09-134-001C-3126
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                                                    ; ORGANISM: ACLINE
US-09-328-352-6079
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Sequence 9552, Application US/09489039A
Fatent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY BECON et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
FRICR APPLICATION NUMBER: US 60/117,747
FRICR APPLICATION NUMBER: US 60/117,747
FRICR PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
          66 GNGDREPGFGSSERLLGQILATDLKPYRDELVISTKVG-YEIHPGPYGVGTSRKAVIQGL 124
                                                                                                                                             -----DIFT-YVLDRVPPGTVDVILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLA 213
                                                                                                                                                                                                                                                                                                                                                                                                                 231 EGLLSDRYLKGIPDTFKIHPTNKATFAKGKBAVVKQLNALNBIAH--DRDQTLSQMALAW 288
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                                                                                                           DESLERLQLDYVDILHCHDIBFGSLDQI-VSETIPALQKLKQEGKTRFIGITGLPL----
                                                                                                                                                                                                                                                                             181 BAIAMFKDLHTPFVLNQ------YSYNMFNRTAET-SGLIDALKADGAGLIAYGPLS
                                                                                                                                                                                                                                                                                                                                                                              214 MGLLTE---QGPPEW---HPASPELKSASKAAV-----AHCKSKGKKITKLALQY
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Best Local Similarity 27.7%
Matches 101; Conservative
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US-09-489-039A-9552
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAB FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRNCE: 2709, 2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12541
LENGTH: 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G---GTLSEKMLGKGLKALQVP-RSDYIVATKCGRYKEGFDFSAERVRK----SIDESLE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 NDLGTPCIIHQPR-----YSMPERGVEEG----LLDFLQTEGIGSIAFSPLAGGQLTDR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 YLNGIPADSRAASSSRFLQPEQLTPARLEKIRQLNRQA----EARGQKLSQMALAWVLRE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GG-----TLSEKMLGKGLKA-LQVPRSDYIVATKCGRYK-----EGFDFSAERVRKSI 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GPPEWHPASPE-LKSASKAAVAHCKSKGKKITKLALQYSLAN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 IELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVRE----AFRLGINFFDTSPYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 -DIFTYVLDRVPPGTVDVILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KIBLRALGNTGLKVSAVGFGA-SPLGSV--FGPVAEDDAVATVREAFRLGINFFDTSPYY
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17.1%; Score 277; DB 4; Length 334;
Best Local Similarity 27.7%; Pred. No. 1.8e-20;
Matches 96; Conservative 74; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 KEISSVLVGMSSVSQVEENVAAVTELESLGMDQETLSEVEAIL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 86, Application US/09724623
Patent No. 6476209
GENERAL INFORMATION:
GENERAL INFORMATION:
Matthew
APPLICANT: Lubbers, Mark W
APPLICANT: Lubbers, Mark W
APPLICANT: Lubbers, Mark W
APPLICANT: Dekker, James
TITLE OF INVENTION: Polynucleotides, materials incorr
TITLE OF INVENTION: them, and methods for using them.
FILE REFERENCE: 104801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
17.1%; Score 277.5; DB 4;
Best Local Similarity 28.6%; Pred. No. 1.9e-20;
Matches 98; Conservative 71; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/724,623
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 124
SECTIARRE: FastSEQ for Windows Version 4.0
SEQ ID NO 86
LENGTH: 334
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                                                                                                                                                                                                                                                                                                                                                                       GRGANISM: Klebsiella pneumoniae US-09-489-039A-12541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----
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US-09-724-623-86
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Patent No. 6610836

GENERAL INFORMATION

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/489, 039A

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT PILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747
                                                                                                                                                                                                                 :|::|| :||:|| :||:|| 88 SNEELLG---EALRGKREQVFLASKFGIVRDPANPRARGVDGSPAYIRRAIEGSLKRLGT 144
                                                                                                                                                                                                                                                                                                     DYVDILHCHDIEFGSLDQI-VSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPG 174
                                                                                                                                                                                                                                                                                                                                               175 TVDVILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLT------EQGPPEWHP 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 ASP-----ELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLDYVDILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLP-LDIFTYVLDRVP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 173 PGTVDVILSYCHYGVNDSTL-LDLLPYLKSKGVGVISASPLAMGIL------TEOGP 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 PEWHPASPELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVA 282
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                                                                                                28 MKTRQLGHNGPSVSAIGLGCMGMTDFYTTGGDRQBAIATLHRAVBLGLNFFDTADMYGPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 LSEKMLGKGLKALQVPRSDYIVATKCGRYKE-----GFDFSAERVRKSIDESLERLQL
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                                                      4 IELRALGNTGLKVSAVGFGASPLGSVFGPVAE-DDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYY-----
Gaps
40;
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Indels
60; Mismatches 133;
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ENVAA-TELR---LSAAELAELDAI 337
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US-09-489-039A-9489
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illarity 27.5%;
Conservative 61
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SEQ ID NO 9489
Conservative
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Best Local Similarity
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US-09-489-039A-9489
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Facture No. 6551795

GENERAL INFORMATION:
FAREAL INFORMATION:
TILLE OF INVENTION:
TILLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

FRIOR APPLICATION NUMBER: US 60/074,788

FRIOR APPLICATION NUMBER: US 60/094,190

FRIOR FILING DATE: 1998-02-18

FRIOR PELING DATE: 1998-02-18

FRIOR FILING DATE: 1998-02-18

FRIOR PILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 258
                                      Sequence 12803, Application US/09489039A

Sequence 12803, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-29

RIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12803

LENGTH: 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 SEEIVGRALRDF-ARRDEVVVATKVYHQVGDLAEG--LSRAQIILRSIDDSLRRLGMDYVD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 ILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLD-RVPPGTVDV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 ILSYCHYG-VNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASK 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KITKLALQYSLANKEISSVLVGMSSVSQVEEN 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 igdtalrvsricigcmifgepdrgrhawtipeessrplighaieginffdtansysdgs 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| | :: : : | | :: | | : | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 LGNTGLKVS----AVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEKMLGKGLKALQVPRSDYIVATK----CGRYKEGFDFSAERVRKSIDESLERLQLDYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.3%; Score 264; DB 4; Length 358; 28.3%; Pred. No. 4.8e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 271; DB 4; 27.9%; Pred. No. 7.6e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 VAAVTELESLGMDOETLSEVEAILEP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
-09-252-991A-31535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      238 AAVAHCKSK-----GK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 27.9
Matches 91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                US-09-489-039A-12803
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317 ATT----ITLSDDIMSCLDBI-----WP 335

Search completed: November 13, 2005, 08:39:24 Job time : 29 secs

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Sequence 8943, Ap Sequence 21813, A Sequence 21817, A Sequence 45565, A Sequence 45565, A Sequence 45565, A Sequence 57831, A Sequence 71604, A Sequence 71604, A Sequence 71604, A Sequence 15672, Sequence 15672, Sequence 15673, A Sequence 15673, A Sequence 15673, A Sequence 15673, A Sequence 15673, A Sequence 15673, A Sequence 15673, A Sequence 55914, A Sequence 57996, 
Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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61 GTLSEKMLGKGLKALQVPRSDYIVATKCGRYKEGFDFSAERVRKSIDESLERLQLDYVDI 120
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4 US-10-156-761-8943

4 US-10-156-761-14013

5 US-10-36-493-21187

5 US-10-37-963-171001

5 US-10-425-115-488

6 US-10-425-115-488

6 US-10-425-115-488

6 US-10-425-115-488

6 US-10-369-493-7635

8 US-10-369-493-7635

8 US-10-369-493-7635

9 US-10-282-122A-57813

10 US-09-815-242-10186

10 US-09-815-242-10186

10 US-09-815-242-493-862

10 US-09-815-242-11846

10 US-09-812-242-11846

10 US-09-812
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Pred. No. 1.3e-149;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/10240136A
Publication No. US2004005325A1
GENERAL INFORMATION:
APPLICANT: ABCOLOSE Limited
TILE PREFERINCE: JPD/PLO6066US-PCT
CURRENT APPLICATION NUMBER: US/10/240,136A
CURRENT FILING DATE: 2003-07-14
PRIOR PILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
ILENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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Best Local Similarity 100.0%;
Matches 319; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Arabidopsis thaliana
US-10-240-136A-5
        301.5
300.5
297.5
297.5
296.5
294.5
        385
368.5
337.5
329.5
329.5
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307.5
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Sequence 11, Appl
Sequence 262305,
Sequence 279899,
Sequence 279899,
Sequence 279897,
Sequence 279897,
Sequence 28023, A
Sequence 4049, A
Sequence 4046, Ap
                                                                                                                                                                                ; Search time 78 Seconds (without alignments) 1711.187 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                         1 MTKIELRALGNTGLKVSAVG.....VBAILEPVKNLTWPSGIHQN 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10P_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.ppp:*
| cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.ppp:*
| cgn2_6/ptodata/1
                                  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-606-300-11
US-10-424-59-262305
US-10-424-13940
US-10-425-115-279898
US-10-425-115-279897
US-10-425-115-279897
US-10-425-114-69240
US-11-097-143-28023
US-11-097-143-4479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1867879 segs, 418409474 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                   November 13, 2005, 08:35:38
                                                                                                                                     Bw model
                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                     - protein search, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                   US-10-606-300-11
1619
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Match Length DB
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Sequence

120

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1619 1619 1279 1279 1199.5 1199.5 1191.5 593.6 593.6 544.5

Score

Result No.

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Length 319;

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US-10-17-963-113940

Sequence 113940, Application US/10437963

Sequence 113940, Application US/10437963

Sequence 113940, Application US/10437963

Publication No. US2004012334341

SEQUENCE INFORMATION:

APPLICANT: La Rosa Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Bukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Rice Nucleic Acid Molecules Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221) B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 113340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GTLSEKMLGKGLKALQVPRSDYIVATKCGRYKEGFDFSAERVRKSIDESLERLQLDYVDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    197 SYCHYCVNDTSLGELVPYLKTKGVGIINASPLSMGLLTESGPPEWHPASLELKSACQAAA 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGMDQETLSEV 300
                                                                                                                                                                                                                                                                                                                                                                                                  181 SYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MTKIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYG
Plants and Uses Thereof for Plant Improvement
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US-10-437-963-113940
                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_78884C.1.pep
US-10-424-599-262305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 74.9%; Score 1213; DB 16; Best Local Similarity 74.3%; Pred. No. 7.6e-110; Matches 234; Conservative 29; Mismatches 52;
                                                                                                                                                                                                                                                                                  Query Match 79.0%; Score 1279; DB 15; Best Local Similarity 76.8%; Pred. No. 2.8e-116; Matches 245; Conservative 37; Mismatches 37;
                    FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
ESQ ID NO 262305
LENGTH: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 EAILKPVKNOSWPSGIOOS 335
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                                                                                                                                                                           ORGANISM: Glycine max
  TITLE OF INVENTION:
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Publication No. US20040031072A1
GENERAL INFORMATION: US20040031072A1
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                               241 AHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGMDQETLSEV 300
                                                                                                                                                         241 AHCKSKGKKITKLALQYSLANKEISSVIVGMSSVSQVEENVAAVTELESLGMDQETLSEV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTLSEKMLGKGLKALQVPRSDYIVATKCGRYKEGFDFSAERVRKSIDESLERLQLDYVDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVDVIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGMDQETLSEV 300
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  LHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVDVIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTKIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYG 60
                                                                  181 SYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAAV
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                                                                                                                                                                                                                                                                                                                           RESULT 2
US-10-606-300-11
; Sequence 11, Application US/10606300
; Publication No. US20050019879A1
; GENERAL INFORMATION:
; APPLICANT: Forro, Danilo
; TITLE OF INVENTION: Ascorbic Acid Production from Yeast
; FILE REFERENCE: 2028.594000
; CURRENT APPLICATION NUMBER: US/10/606,300
; CURRENT APPLICATION NUMBER: US/10/606,300
; CURRENT PILING DATE: 203-06-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
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100.0%; Score 1619; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-149;
Matches 319; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                               EAILEPVKNLTWPSGIHON 319
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                                                                                                                                                                                                                      EAILEPVKNLTWPSGIHON 319
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; ORGANISM: Arabidopsis thaliana
US-10-606-300-11
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US-10-424-599-262305
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RESULT 6
US-10-767-701-44783
Sequence 44783, Application US/10767701
Sequence 44783, Application US/10767701
Sequence 44783, Application WS. US20040172684A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
STILE OF UND DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NOS: 63128
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant and the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structur
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Best Local Similarity 73.7%; Pred. No. 1.7e-108;
Matches 233; Conservative 32; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C59142_1.pep
US-10-767-701-44783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 279897, Application US/10425115; Publication No. US20040214272A1; GENERAL INFORMATION:
301 ILEPVKNLTWPSGIQQ 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 ILEPVKNLTWPSGIHQ 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Sorghum bicolor
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US-10-425-115-279897
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US-10-25-115-279898
US-10-25-115-279898
US-10-279898, Application US/10425115
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                                                                                                                                                                                                                                                   124 HDIBFGSLDQIVSETIPALQKLKQBGKTRFIGITGLPLDIFTYVLDRVPPGTVDVILSYC 183
121 HDIEFTDLDQIVNETIPVLQKIKESGKARFIGITGLPLSIYTYVLDQVPPGSVDVILSYC 180
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   4 IBLRALGNTGLKVSAVGFGASPLGSVPGPVAEDDAVATVREAFRLGINFFDTSPYYGGTL 63
                                    61 SESVLGDCLRAAGVPRDRFVVATKCGRYREGFDFSAARVTRSVDESLARLGLDYVDILHC
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Best Local Similarity 74.7%; Pred. No. 2.1e-109;
Matches 236; Conservative 29; Mismatches 50; Indels
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    OTHER INFORMATION: Clone ID: MRT4577_186846C.1.pep

US-10-425-115-279898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                         184
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238 AAVAHCKSKGKKITKLALQYSLAN-KEISSVIVGMSSVSQVEENVAAVTELESLGMDQET 296
257 KASEVCKERGVELGKLAMYYTWSGLPEVSTFLTGMQTRQLLRINLDA-NEVGLSDKEQEV 315
123 SMGLLTDNGPPEWHPAPEELKSACKAAADHCRKKGKSITKLAMQYSLMNNEISTVLVGMN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 LSEKMLGKCLKALQVPRSDYIVATKCGRYK----EGFDFSAERVRKSIDESLERLQLDYV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MORE
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| JOHNIAGAL INFORMATION:
| APPLICANT: Venter, J. Craig
| APPLICANT: et al. |
| TITLE OF INVENTION: DETECTION XIT, SUCH AS NUCLEIC ACID |
| TITLE OF INVENTION: DETECTION EXPERSION OF 10,000 OR M |
| TITLE OF INVENTION: DROSOPHILA GENES. |
| TITLE OF INVENTION: DROSOPHILA GENES. |
| TITLE OF INVENTION: DROSOPHILA GENES. |
| CURRENT PILING DATE: 2005-04-04 |
| PRIOR APPLICATION NUMBER: 60/157,832 |
| PRIOR APPLICATION NUMBER: 60/160,191 |
| PRIOR PILING DATE: 1999-10-05 |
| PRIOR PILING DATE: 1999-10-19 |
| PRIOR PILING DATE: 1999-11-12 |
| PRIOR PILING DATE: 1999-11-12 |
| PRIOR PILING DATE: 1999-11-12 |
| PRIOR PILING DATE: 1999-11-12 |
| PRIOR PILING DATE: 1999-11-28 |
| PRIOR PILING DATE: 2000-01-12 |
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| PRIOR PILING DATE: 2000-01-14 |
| PRIOR PILING DATE: 2000-01-15 |
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| PRIOR PILING DATE: 2000-01-16 |
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| PRIOR PILING DATE: 2000-01-17 |
| PRIOR PILING DATE: 2000-01-18 |
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                                                          273 SVSQVEENVAAVTELESLGMDQETLSEVEAILEPVKNLTWPSGIHQ 318
                                                                                            Indels
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42.5%; Pred. No. 4.3e-49;
iive 63; Mismatches 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                    US-11-097-143-28023
; Sequence 28023, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
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Best Local Similarity 42.5'
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: DROSOPHILA US-11-097-143-28023
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Roles Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwar
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21 (53313) B
FILE REFERENCE: 38-21 (53313) B
FILE REFERENCE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 69240
LENGTH: 229
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                                                                                                                                                                                                                                                                                                                                                                                                                       61 SESVLGDCLRHAAVPRDRVVVVATKCGRYKDEGFDFSANRVTRSIDESLARLGLDYVDILH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVDVILSY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AHDIEFTHLEQIVNETIPALQKIKENGKARFIGITGLPLSIYPYVLDRVAPGSVDVILSY 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGM 292
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                                                                                                                                                                                                                 Gaps
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                                                                                                                                                       Length 327;
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                                                                                                                                                                                                              51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: UC-ZMFLB73186H07_FLI.pep
US-10-425-114-69240
                                                                                                                                             Query Match 73.6%; Score 1191.5; DB 16; Best Local Similarity 72.4%; Pred. No. 1e-107; Matches 236; Conservative 28; Mismatches 51; I
                              ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_186845C.1.pep
US-10-425-115-279897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 69240, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
      ORGANISM: Zea mays
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US-10-425-114-69240
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Sequence 8943, Application US/10156761
| Publication No. US20030119018A1
| GENERAL INPORMATION:
| APPLICANT: OMUGA, SATOSHI
| APPLICANT: ISHIKAWA, UUN
| APPLICANT: HORIKAWA, UUN
| APPLICANT: SHIKAWA, UNN
| APPLICANT: SHIRA, TADAYOSHI
| APPLICANT: SARKI, YOSHIVUKI
| APPLICANT: SARKI, YOSHIVUKI
| APPLICANT: HATTOR! MASAHIRA
| TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
| FILE REFERENCE: 249-262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-7146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-10-156-761-8943
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                                                                          APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DERECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, POR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REPERENCE: CLO00728

CURRENT APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR PILING DATE: 1999-10-28

PRIOR PLILNG DATE: 1999-11-28

PRIOR PLILNG DATE: 1999-11-28

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PLILNG DATE: 1999-11-28

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PLILNG DATE: 1999-11-28

PRIOR PLILNG DATE: 2000-01-12

PRIOR PLILNG DATE: 2000-01-12

PRIOR PLILNG DATE: 2000-01-24

PRIOR PLILNG DATE: 2000-01-24

PRIOR PLILNG DATE: 2000-02-24

PRIOR PLILNG DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOCTWARR: FastSEQ for Windows Version 4.0

SEQ ID NO 40479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLSEKMLGKGLKALOVPRSDYIVATKCGRYK----EGFDFSAERVRKSIDESLERLQLDY 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDILHCHDIEFG-SLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 RMBYRQLGSTGLRVSKIALGGATLSKIFSDDFDREEGILTVQEAIRSGINYIDTAPPYGQ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 DVILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 KIELRALGNTGLKVSAVGFGASPLGSVFG-PVAEDDAVATVREAFRLGINFFDTSPYYGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.6%; Score 544.5; DB 2 36.6%; Pred. No. 2.7e-44;
Sequence 40479, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7146, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 LSEVEAILEPV--KNLTWPS 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: : | | :: | | 314 QEVLQYLRENVFTKSYSWGS 333
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Best Local Similarity 36.6
Matches 117; Conservative
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REPERBENCE: CLOOO728
CURRENT PILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/160,192
PRIOR APPLICATION NUMBER: 60/160,193
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PILING DATE: 2000-01-22
PRIOR PILING DATE: 2000-01-22
PRIOR PILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 4300-8
SOFTWARE: PASESEC for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 LSEKMLGKGLKALQVPRSDYIVATKCGRY----KEGFDFSAERVRKSIDESLERLQLDYV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 DILHCHDIEFG-SLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 VILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 AAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGM---DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 26.0%; Score 420.5; DB 20; Length Best Local Similarity 33.7%; Pred. No. 3e-32; Matches 102; Conservative 57; Mismatches 101; Indels
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63

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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FILE REPERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
FRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
                                                                                       ------DFSAERVRKSID 107
                                                                                                          64 GAALR--EHPRTAYTVSTKVGRRLEPTDAGGDDLADGFAVPATHHRVWDFSADGVRRALT 121
                                                                                                                                                                      ESLERLQLDYVDILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYV 167
                                                                                                                                                                                           122 ASLERIGLORVDVVYLHDPD-DHAEQAFREGCPALEKLRSEG---VVGAIGAGMQTAML 177
                                                                                                                                                                                                                                                                              178 TRFVRETDVDVVLCAGRYTLLDQRALADLLPAAADRGTSVVIGGAFNSGLLADPKPGATY 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 MLGKGLKALQVPRSDYIVATKCG-RYKEG-----FDFSAERVRKSIDESLERLQLDYVDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGL-PLDIFTYVLDRVPPGTVDVI 179
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      LGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEKML
                             7 RALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEK
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                                                                                                                                                                                                                                                     168 LDRVPPGTVDVILSYCHYGVNDS-TLLDLLPYLKSKGVGVISASPLAMGLLTEQGPP---
                                                                                                                                                                                                                                                                                                                                    224 EWHPASPELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEE 279
                                                                                                                                                                                                                                                                                                                                                             238 NYAAAPPELLDRALRIKAVAERHGTTLRGAALAFCAAHPAVASVLVGARSPYEVRD 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 LSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPAS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-369-493-23187
; Sequence 23187, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
                                                                                       GKGLKALQVPRSDYIVATKCGRYKE-
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                                                                                                                                                                                                                                                                          Length 328;
                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OVEENVA-AVTELESLGMDQETLSEVEAILEPVKNLTWPSGI 316
                                                                                                                                                                                                                                                                        23.8%; Score 385; DB 14; I
29.5%; Pred. No. 1.1e-28;
ive 68; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR PILING DATE: 2001-08-02
NUMBER: OF SEQ ID NOS: 15109
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
FRIOR APPLICATION NUMBER: UP 2001-204089
FRIOR PLING DATE: 2001-05-30
FRIOR PILING DATE: 2001-08-02
FRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 8943
LENGTH: 328
TYPE: PRI
ORGANISM: Streptomyces avermitilis
US-10-156-761-8943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-10-156-761-14813
; Sequence 14813, Application US/10156761
; Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Streptomyces avermitilis US-10-156-761-14813
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Matches 101; Conservative
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LENGTH: 328
TYPE: PRT
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Sequence 171001, Application US/10437963
; Sequence 171001, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Yihua
; APPLICANT: Cao, Yogwei
; APPLICANT: Roukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Brandaruk, Brad
; APPLICANT: Brandaruk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53221)B
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 171001
LENTH: 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 LGKGLKALQVPRSDYIVATKCGRYKEGFDFSA-----ERVRKSIDESLERLQLDYVDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 ILSYCHYGVNDSTLLDLLPYLK--SKGVGVISASPLAMGLLTEQGPPEWHPASPELKSAS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.7 KAAVAHCKSKGK-----VGMSSVS 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                769 ---TRHPRYNGENLEKNKVFYTRIEELATKYGCSPAQLALSWYLHQGDDVVPIPGTTKVK 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 LGNTGLKVSAVGFGASPLGSVF-GPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEKM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

20.7%; Score 335; DB 16; Length 945;
Best Local Similarity 31.5%; Pred. No. 4.3e-23;
Matches 107; Conservative 53; Mismatches 118; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 QVEENVAAVTELESLGMDQETLSEVEAIL----EPVKNL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_69273C.1.pep
US-10-437-963-171001
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Oryza sativa
RESULT 15
US-10-437-963-171001
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Search completed: November 13, 2005, 08:40:50 Job time: 79 secs

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November 13, 2005, 08:30:22 ; Search time 16 Seconds (without alignments) 1918:322 Million cell updates/sec US-10-606-300-11 1619 1 WIKIELRALGNYGLKVSAVG......VEAILEPVKNLTWPSGIHQN 319 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	hypothetical prote	Ω,	D-threo-aldose 1-d	oxidoreductase BH1	hypothetical prote	oxidoreductase Atu		conserved hypothet			hypothetical prote	hypothetical prote	ical	oxid	probable ion-chann	K+ channel, beta s	probable [imported	general stress pro	aldo-keto reductas	m		myo-inositol catab			probable oxidoredu	probable ion chann	aldo/keto reductas	probable reductase	aldo-keto reductas
SUMMARIES	10	T04984	T28841	JC2405	C83776	852890	AF2990	C98293	99669Н	AE2979	H98303	H90938	D85787	C64937	H83427	AB0808	H72391	G95357	D98252	AH3033	AH3156	A98131	D69646	A90688	E85538	C64771	T35337	C97390	11	AD2608
	DB			~																										
	Length	319	439	329	297	335	329	329	306	351	351	326	326	326	323	332	319	338	332	332	353	353	310	324	324	348	319	369	346	333
d	Query Match	100.0	31.1	22.6	22.4	22.1	21.4	21.4	20.8	19.6	19.6	19.4	19.4	19.3	18.9	18.9	18.8	18.8	18.6	18.6	18.4	18.4	18.0	18.0	18.0	18.0	•	•	17.8	17.7
		1619	503	366	362.5	358	346.5	346.5	337.5	317	317	314	314	313	305.5	305.5	305	304.5	301.5	301.5	298.5	298.5	292	291	291	291	290	289	•	287
	60	-	7	٣	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

RESULT 2 T28841 hypothetical protein F37C12.12 - Caenorhabditis elegans

aldo/keto reductas aldo/keto reductas	probable oxidoredu probable oxidoredu	ion channel homolo probable reductase	hypothetical prote sugar-phosphate de	sugar-phosphate de probable oxidoredu	probable aldoketo oxidoreductase [im	oxidoreductase, al	hypothetical prote probable aldo/keto	probable potassium
B75296 AI3183	B86966 AE0554	B69755 B85959	G65086 E82644	D82644 F95403	B95902 D90187	E72284	B96632 AI0341	A75289
0 0	01	7 7	0 0	~ ~	0 0	~	0 0	7
327 338	301 324	310 346	346	362	331 354	379	340 329	315
17.7	17.5	17.5	17.1	17.1	17.0	16.8	16.7	16.6
ທີ່ຕໍ	284 284	283 281.5	277.5	276.5	274.5	271.5	270.5	268.5
286.5		N						

## ALIGNMENTS

RESULT T04984 hypoth C;Spec	RESULT 1 174984 Propthetical protein T16L1.160 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C;Date	C.Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
R; Beva	RiBevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W.;
A; Refe	Authorities to the factor of t
A; Mole	A;Accession: 10,20% A;Molecule type: DNA
A, Resi	A;Residues: 1-319 <bev></bev>
A, Expe	A)Experimental Bource: cultivar Columbia, BAC clone T1611
C, Genetics: A: Map posit	C;Genetics: A:Map position: 4
A, Intr	A; Introns: 57/2; 133/3; 233/3; 276/3
A;Note C;Supe	A,Note: T1611.160 C,Superfamily: fission yeast pyridoxine 4-dehydrogenase
Quer	Query Match 100.0%; Score 1619; DB 2; Length 319;
Best	100.0%; .ative 0;
ò	1 MTKIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYG 60
ą	1 MIXIELRALGNIGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYG 60
È	61 GTLSEKMIGKGLKALQVPRSDYIVATKCGRYKEGFDFSAERVRKSIDESLERLQLDYVDI 120
අ	61 GTLSEKMLGKGLKALQVPRSDY1VATKCGRYKEGFDFSAERVRKSIDESLERLQLDYVDI 120
ò	121 LHCHDIBFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDIFTYVLDRVPFGTVDVIL 180
ą	121 LHCHDIBFGSLDQIVSBTIPALQKLKQBGKTRFIGITGLPLDIFTYVLDRVPPGTVDVIL 180
ò	181 SYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAAV 240
qa	181 SYCHYGVNDSTLIDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPELKSASKAAV 240
ò	241 AHCKSKGKKITKGALQYSLANKBISSVLVGMSSVSQVBENVAAVTBLBSLGMDQETLSBV 300
QQ	241 AHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENVAAVTELESLGMDQETLSEV 300
ò	301 EALLEPVRALTWPSGIHQN 319
QQ	301 EAILEPVKALTWPSGIHQN 319

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oxidoreductase BH1011 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: C83776
A;Ratani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirk Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83550; MUID:20512582; PMID:11058132
A;Rature preliminary
A;Residues: 1-297 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9KE47; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB047
A;Experimental source: strain C-125
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236
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                                                                                                                                                                               103
                                                                                                                                                                                                                 67 IGAFLQT--KPRDEFVVSTRAGRILRPNPERRPSGLDTDNDFHVPDDLRREWDFTEQGIR 124
                                                                                                                                                                                                                                                                                                            163
                                                                                                                                                                                                                                                                                                                                           217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LHCHDIEFGSLDQIVSETIPALOKLKQEGKTRFIGITGLPLDIFTYVLDRVPPGTVDVIL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 SYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPE----WHPASPELKSAS 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                      67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 LTRA---VREADLDLIMVAGRY----TLLEQPAATEVLPACAENATGIVAASVFNSGLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 RQLGTSDLHVSELGFGCMSLGT----DETKARRIMDEVLELGINYLDTADLYNQGLNEQ
                                                                                 7 AAAAAGLAIPALGYGAANVGNLFRALSDDEAWAVLEAAWDAGIRYYDTAPHYGLGLSEKR
                                                                                                                                                                                                                                                                                                            104 KSIDESLERLQLDYVDILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITGLPLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 TEQGPP-----EWHPASPELKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMS
                                               8 ALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGTLSEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                   164 FTYVLDRVPPGTVDVILSYCHYGVNDSTLL-----DLLPYLKSKGVGVISASPLAMGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: BH1011
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 RPAQLIQNAEYAALEIPA-GLWAE-LAEARLIPTP 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVSQVEENVA-AVTELESLGMDQETLSEVEAILEP 306
                                                                                                                                                                                   LGKGLKALQVPRSDYIVATKCGR
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Matches
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Cipacies: Pseudomonas sp.
Cipacies: Pseudomonas sp.
Cipacies: Pseudomonas sp.
Cipacies: Pseudomonas sp.
Cipacies: V4.Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
Cipacession: JC2405; PC250
Rivamanoto-Otake, H.; Nakano, E.; Koyama, Y.
Biosci. Biotechnol. Biochem. 58, 2281-2282, 1994
A;Title: Cloning and sequencing of the L-fucose dehydrogenase gene from Pseudomonas sp.
A;Title: Cloning and sequencing of the L-fucose dehydrogenase gene from Pseudomonas sp.
A;Title: Cloning and sequencing of the L-fucose dehydrogenase gene from Pseudomonas sp.
A;Reference number: JC2405, MUID:95128037; PMID:7765723
A;Accession: JC2405
A;Residues: 1-329 «YAM.>
A;Residues: 1-329 «YAM.>
A;Cross-references: UNIPROT:Q52472; DDBJ:D32042; NID:g829053; FIDN:BAA06803.1; PID:g8296
A;Accession: PC2250
A;Molecule type: protein
A;Residues: 2-31;147-171;181-195;199-214 «YAM2>
C;Comment: This enzyme is NADPH specific.
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
C;Comment: This enzyme is NADPH specific.
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
F;21-31/Region: NADP binding #status predicted
                C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28841
R;Fulcon, L.
B;Fulcon, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 RMNYRQIPGTDIRMSKIGFGAAAIGGMFGNV-EDSIIKIVETAIKQGINYIDTGYMYSQS 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 LSEKWLGKGLKALQVPRSDYIVATKCGR----YKEGFDFSAERVRKSIDESLERLQLDYV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 RSESILGKALS--KIPRKAYYISTKVGRFELDYARTFDFRADKILESLTNSLKRLQLTYI 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 PPGTVDVILSYCHYGVNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPPEWHPASPE 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKSASKAAVAHCKSKGKKITKLALQYSLANKEISSVLVGMSSVSQVEENV----AAVTE 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DI--LHCHDIEFGSLDQIV-SETIPALQKLKQEGKTRFIGITGLPLD----IFTYVLDRV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
'Species: Caenorhabditis elegans
pate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
Accession: T28841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 KIELRALGNTGLKVSAVGFGASPLGSVFGPVAEDDAVATVREAFRLGINFFDTSPYYGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: CESP:F37C12.12
A;Map position: 3
A;Introns: 31/3; 63/3; 101/1; 127/1; 148/3; 204/3; 268/3; 312/3; 371/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
31.1%; Score 503; DB 2; Length 439;
Best Local Similarity 36.8%; Pred. No. 4.3e-30;
Matches 120; Conservative 58; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 329;
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22.6%; Score 366; DB 2; Length 32
Best Local Similarity 30.7%; Pred. No. 5.6e-20;
Matches 103; Conservative 62; Mismatches 122; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-threo-aldose 1-dehydrogenase (EC 1.1.1.122)
N;Alternate names: L-fucose dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LESLGMDOETLSEVEAILEPVKNLTW 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *| | : : : | | VEQRVEDR----IMRRYLDELENAGW 381
                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
Gene: CESP:F37C12.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
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D-three-aldose 1-dehydrogenase (EC 1.1.1.122) [imported] - Agrobacterium tumefaciens (st C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Accession: C58293
R;Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, R.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q8UA47; GB:AE007870; PIDN:AAK89869.1; PID:g15159812; GSPDB:(
                                                                                           61 SERRYGDFLQ--EKPRDEFVLSTKYGRILKPAEAGYTPDYGFVDALPFIVEYDYSYDGIM 118
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                                                                                                                                                                                                                                                                                                                                                                            209 ASPLAMGLLTEQGPP----EWHPASPELKSASKAAVAHCKSKGKKITKLALQYSLANKEI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| | | : | | : | | :: | | | :: | | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :
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30.1%; Pred. No. 1.6e-...
-4ve 64; Mismatches 120;
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Matches 102; Conservative
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C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C; Accession: AF2990
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.R.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Bit. E.W.
A; Tille: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2577; MUID:21608550; PMID:11743193
A; Retus: preliminary
A; Molecule type: DNA
A; Retus: preliminary
A; Molecule type: DNA
A; Residues: 1-329 < KURN>
A; Cross-references: UNIPROT:QBUA47; GB:AE008689; PIDN:AAL44340.1; PID:g17741932; GSPDB:G
A; Experimental source: strain C58 (Dupont)
hypothetical protein YMR041c - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein YM9532.06c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S52890
R;Odell, C.; Bowman, S.
Bubmitted to the EMBL Data Library, February 1995
A;Reference number: S52895
A;Reference number: S52895
A;Reference number: S52896
A;Reference number: S52896
A;Reference number: S52896
A;References: UNIPROT:Q04212; EMBL:Z48502; NID:g695715; PIDN:CAA88407.1; PID:g6957
C;Genetics:
C;Genetics:
A;Gene: MIPS:YMR041c
A;Gene: MIPS:YMR041c
A;Gene: MIPS:YMR041c
A;Gene: MIPS:YMR041c
A;Gene: MIPS:YMR041c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42 VREAFRIGINFFDISPYYGGILSEKMIGKGLKAL--QVPRSDYIVATKCGRY-KBGFDFS
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Best Local Similarity 32.6%; Pred. No. 2.3e-19;
Matches 97; Conservative 57; Mismatches 112; Indels
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; Pred. No. 1.6e-18;
64; Mismatches 120;
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Best Local Similarity 30.1%;
Matches 102; Conservative 6.
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Gene: Atu3528
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hypothetical protein AGR L 2777 [imported] - Agrobacterium tumefaciens (strain C58, Cere C; Species: Agrobacterium tumefaciens C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
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CiSpecies: Agrobacterium_Tümefaciens
CiDate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
CiDate: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
E; Accession. H99303
R;Godner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; MUID:21608551; PMID:11743194
A; Accession: H99303
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                               A;Cross-references: UNIPROT:Q8UAD6; GB:AE008689; PIDN:AAL44251.1; PID:g17741835; GSPDB:CA;Experimental source: Etrain C58 (Dupont)
C;Genetics:
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A;Cross-references: UNIPROT:Q8UAD6; GB:AE007870; PIDN:AAK89954.1; PID:g15159913; GSPDB:C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 ILHCHDIBFGSLDQIVSETIPALQKIKQEGKTRFIGIT----GLPLDIFTYVLDRVPPGTV 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             351;
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19.6%; Score 317; DB 2; Length 35
Best Local Similarity 29.8%; Pred. No. 2.9e-16;
Matches 101; Conservative 60; Mismatches 128; Indels
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           A; Reference number: AB2577; MUID:21608550; PMID:11743193
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A,Map position: linear chromosome
C,Superfamily: fission yeast pyridoxine 4-dehydrogenase
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AjMap position: linear chromosome
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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                                                 A;Accession: AE2979
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-351 <KUR>
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Matches 101;
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H69966

Conserved hypothetical protein yqkF - Bacillus subtilis

Cispecies: Bacillus subtilis

Cispecies: Bacillus subtilis

Cispecies: Bacillus subtilis

Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

Cispecies: Bacillus subtilis

Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

Cispecies: Bacillus subtilis

Cispecies: Bacillus subtilis

Cispecies: Bacillus subtilis

Cispecies: Bacillus subtilis

A: Ehrlich, S. D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Natures: 390, 249-256, 1997

A: Ehrlich, S. D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler

iech, J.; Harold, S.; Krogh, S.; Kumano, M.; Kuita, K.; Lapidus, A.; Latinois,

A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Satonon,

A; Authors: Schleich, S.; Schroeter, R.; Scoffone, E.; Sekiguchi, J.; Sekowska, A.; Serot

A; Winters, P.; Winters, P.; Wimpat, A.; Yamameno, W.; Yasumoto, K.; Yasumot
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C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2979
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Levy, R.; Li, M.; McClell
F, Karp, P.; Romerro, T.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P54569; GB:Z99116; GB:AL009126; NID:g2634723; PIDN:CAB14294.
A;Experimental source: strain 168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
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Best Local Similarity 31.3%; Pred. No. 7e-18;
Matches 100; Conservative 64; Mismatches 108; Indels 47; Gaps
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Superfamily: fission yeast pyridoxine 4-dehydrogenase
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A; Status: preliminary; nu
A; Molecule type: DNA
A; Residues: 1-306 «KUN»
A; Residues: UNIPR
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D.J.; Mayher,
K.; Apodaca,
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-326 <BLAT>
A;Cross-references: UNIPROT:P77256; GB:AE000272; GB:U00096; NID:g1788067; PIDN:AAC74841.
A;Cross-references: Strain K-12, substrain MG1655
C;Superimental source: strain K-12, substrain 4-dehydrogenase
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RyBlattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Ttle: The complete genome sequence of Escherichia coli K-12.
A;Recesence number: A64720; MUID:97426617; PMID:9278503
A;Accession: C64937
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Accession: D85787

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, Iiler, L.; Grocheck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Status: preliminary

A;Status: DNA

A;Residues: 1-326 <STO>
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C;Species: Escherichia coli
C;Datte: 12-26p-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: C64937
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland. V.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 SPYYGGTLSEXMLGKGLKALQVPRSDYIVATKCG------
                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: 22809
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 TEQGPPEWHPASPELKSASKAAVAH-
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Best Local Similarity 30.0%;
Matches 103; Conservative 46
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Matches 103; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              Gene: Z2809
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D85787
Mypotherical protein Z2809 [imported] - Escherichia coli (strain O157:H7, substrain
C;Species: Bscherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                               GDKRVLETEWRPESVEI--AQKVA-AHAASKGVSAADFALAWVLNNKFVTAAITGPRTEE 287
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                                                                                                                                               DVILSYCHYG-VNDSTLLDLLPYLKSKGVGVISASPLAMGLLTEQGPP---
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Species: Pseudomonas acruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83427
R;Stover. C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Recession: H83427
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: L323 <STO>
A;Cross-references: UNIPROT:Q91228; GB:AE004600; GB:AE004091; NID:g9947712; PIDN:AAG0512
A;Experimental source: strain PA01
C;Generics:
A;Gene: PA1739
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                      probable oxidoreductase PA1739 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #semiense zeriginosa c; --- ---- ...
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                                                     AERVRKSIDESLERLQLDYVDILHCHDIEFGSLDQIVSETIPALQKLKQEGKTRFIGITG 158
                                                                            ----CKSKGKKITKLALQYSLAN 261
                                                                                                                                                                                                                                          226 İGTITRDYYPGGAR---ANKVWFQRENMLKVIDMLEQWQPLCARYQCTİPTLALAWILKQ 282
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                                                                                                                                                      6 LGNSGLKVSRLCLGCMTYGDPAWRPWVLDEERARPFIREALEAGIDFFDSADIYSTGESE
                                                                                                                               159 LPLDIFTYVLDRVPPGTVDVILSYCHYGVNDSTL-LDLLPYLKSKGVGVISASPLAMGLL
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Gene: PA1739
:Superfamily: fission yeast pyridoxine 4-dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 18.9%; Score 305.5; DB 2; Best Local Similarity 29.1%; Pred. No. 1.9e-15; Matches 95; Conservative 57; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENVAAVTELESLGMDOETLSEVEAIL 304
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RESULT 15 AB0808

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probable ion-channel protein STY2647 [imported] - Salmonella enterica subsp. enterica se c'species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi c;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AB0808 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Heference number: AB0502; WUID:21534947; PMID:11677608 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Accession: AB0808 A;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL513382; PIDN:CAD07644.1; PID:g16503631; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           114
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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Matches 101; Conservative
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Protein e Pseudomon

**BLOSUM62** 

Scoring table:

Total number Minimum DB Maximum DB M

Searched:

Perfect score:

Sequence:

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Protein

Bacterial

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                                                                                                                                             E. coli Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel L-galactose dehydrogenase protein and nucleic acid sequence encoding the protein for producing genetically modified plants and microorganisms with enhanced ability to synthesize ascorbic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana L-galactose dehydrogenase (L-galDH) protein.
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ABU16921
ABU42693
ABP38281
ADS04717
ABU34174
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ID AAE11998 standard; protein; 319 AA
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N-PSDB; AAD19526.
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-MODEL=frame+ n2p.model -DEV=xlh
-MODEL=frame+ n2p.model -DEV=xlh
-MODEL=frame+ n2p.model -DEV=xlh
-C=CgnZ_1/USFDC_spool h/USI0606300/runat_07112005_094818_7295/app_query.fasta_1.1159
-DEV_CGnZ_1/USFDC_spool h/USI0606300/runat_07112005_094818_7295/app_query.fasta_1.1159
-DEV_CGNZ_1 = STRAT=1 = NDD=-1 -MATRIX=DOSUMG2 -TRANS=human40.cdi -LIST=45
-UNITS=blts -STRAT=1 = NDD=-1 -MATRIX=100 -THR NIN=0 -ALIGN=15 -MODE=LOCAL
-UNTRAT=ptc -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXICH=200000000
-USER=USI0606300 @CGN 1 1 101 @runat_07112005_094818_7295 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGS_CGNSES=0 -MAIT -DSPBADCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                         protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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AAG16520
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Length

Query

Score

Result

Database :

319 319 319 319 342 329 329 306

97.9 96.8 96.8 33.9 33.9 225.4 20.5 20.5

1619 1619 1600 1286 593.5 544.5 420.5 339.5

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The invention relates to generating ascorbic acid or its salt, involves obtaining a recombinant yeast capable of converting an ascorbic acid precursor into ascorbic acid, culturing the recombinant yeast in a medium comprising an ascorbic acid precursor, thus forming ascorbic acid, and isolating the ascorbic acid. Also include are stabilising ascorbic acid and accorbic acid or its salt and a recombinant yeast functionally ascorbic acid or its salt and a recombinant yeast functionally carniformed with a coding receive dehydrogenase (LGDH), L-galactono-1, 4 lactone dehydrogenase (RGD). D-arabinose dehydrogenase (RGD), D-arabinose dehydrogenase (RD), carbinono-1, 4-lactone oxidase (RD), carbinono-1, 4-lactone oxidase (RD), carbinono-1, 4-lactone oxidase (RD), carbinose dehydrogenase (RD) activity, where the recombinant yeast is capable of converting to ascorbic acid at least about 25% ascorbic acid precursor or is capable of producing at least 20 mg ascorbic acid precursor. The yeast is cultured in a medium comprising one ascorbic acid precursor. The ascorbic acid precursor. The ascorbic acid precursor.
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221
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                                The present invention relates to an isolated protein having L-galactose dehydrogenase (L-galbH) biological activity. L-galbH uncleic acid is useful for generating transgenic organisms and modified pants with enhanced ability to synthesise ascorbic acid. L-galbH facilitate the production of a plant that has been genetically modified to express a mutated L-galbH protein which is resistant to herbicides that act against the naturally occurring L-galbH and to identify and/or design compounds that are inhibitors of L-galbH and to identify and/or design compounds therbicide which acts on L-galbH and damages or kills plants that express the enzyme. The present sequence is Arabidopsis thalian L-galactose dehydrogenase (L-galbH) protein. The L-galbH gene is located on
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Claim 1; Page 57-58; 58pp; English
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                                                                                            241 AlaHisCysLysSerLysGlyLysLysIleThrLysLeuAlaLeuGlnTyrSerLeuAla
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                                                       GCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A. thaliana L-galactose dehydrogenase (LGDH).
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281 ValAlaAlaValThrGluLeuGluSerLeuGlyMetAspGlnGluThrLeuSerGluVal 300
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deficiency of which causes scurvy in humans. The present sequence represents A. thaliana LGDH
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Mismatches:
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
GAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGTGGAATCCATCAGAAC 957
                                                                                                                                                                                             Arabidopsis thaliana protein fragment SEQ ID NO: 17197.
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                                                                                               AAG16520 standard; protein; 357
                                                                                                                                                                                                                                                                                                                                                                                                                      9905-0121825P.
9905-0123180P.
9905-012578BP.
9905-012678P.
9905-012678P.
9905-012674P.
9905-0120714P.
9905-013049P.
9905-013049P.
9905-0130487P.
9905-0132487P.
9905-013221P.
9905-0134221P.
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99US-0139452P.
99US-0139453P.
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99US-0148684P.

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RR 18-UN-1999 9908-01394554P
RR 18-UN-1999 9908-0139455P
RR 18-UN-1999 9908-0139462P
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RR 22-UN-1999 9908-014339P
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357 317 1 0 0

US-10-606-300-12 (1-960) x AAG16520 (1-357)

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence:
                                                                              990S-0121825P.
990S-0123180P.
990S-012548P.
990S-012548P.
990S-012648P.
990S-012678P.
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                             Arabidopsis thaliana
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11 - JUN - 1999;
16 - JUN - 1999;
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                                                                        AACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGA 242
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62
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                                                CGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACACCCCCCGTATTATGGAGG
                                                                                                 aLeuGlnLysLeuLysGlnGluGlyLysThrArgPheIleGlyIleThrGlyLeuProLe
GACGAAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCCGTTGGTTT
      AGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGCCTTCAGCTTGATTATGTTGACATACT
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RR 24-JUN-1999; 99US-0140134P.

RR 26-JUN-1999; 99US-0140184P.

RR 26-JUN-1999; 99US-0140184P.

RR 10-JUL-1999; 99US-014184P.

RR 11-JUL-1999; 99US-014184P.

RR 22-JUL-1999; 99US-014632P.

RR 22-JUL-1999; 99US-014638P.

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|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | Length: Matches: Conservative: Mismatches: Indels: Gaps:     | (1-253)           |
| 99US-0151438P. 99US-0151930P. 99US-0151930P. 99US-015203P. 99US-015403P. 99US-015403P. 99US-0154139P. 99US-0155139P. 99US-0155559P. 99US-0155559P. 99US-0155559P. 99US-015553P. 99US-015553P. 99US-0155239P. 99US-0155239P. 99US-0155239P. 99US-0155239P. 99US-0155239P. 99US-0155239P. 99US-0155239P. 99US-0155239P. 99US-0155239P. 99US-015533P. 99US-015533P. 99US-015533P. 99US-015539P. 99US-015539P. 99US-015539P. 99US-015539P. 99US-015539P. 99US-015539P. 99US-015539P. 99US-01559P. | 1.3<br>128<br>100<br>ty: 100<br>3                            | 960) x AAG16521   |
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| ***************************************                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Aligni<br>Pred.<br>Score<br>Perces<br>Best J<br>Query<br>DB: | US-1              |

GACGACAGCTTCGGAGGCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGACATT 378

258

ATGCTTGGTAAGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGGCTACT

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GAGTTCGGGTCTTTGATCAGATTGAAAACAATTCCTGCTCTTCAGAAACTGAAA 438

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GCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATAC
   US-10-606-300-12 (1-960) x ABB67077
  1.32e-54
593.50
63.46%
42.52%
35.90%
  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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   Sequence 345
  Alignment Scores:
Pred. No.:
   217
  118
  67
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   detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
   GGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAGATTTCGTCG
                           GInGluGlyLygThrArgPheIleGlyIleThrGlyLeuProLeuAspIlePheThrTyr
   GITCITGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGC
   ValLeuAspArgValProProGlyThrValAspVallleLeuSerTyrCysH18TyrGly
   GTTAATGATTCGACGTTGCTGGATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTG
   ATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCAC
  CCTGCTTCCCCTGAGGCTCTGCAAGCCAAAGCCGCAGTTGCTCACTGCAAATCAAAG
   Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical.
   Disclosure; SEQ ID NO 28023; 21pp + Sequence Listing; English.
  ValLysAsnLeuThrTrpProSerGly11eHisGlnAsn 253
  GTAAAGAATCTGACATGGCCAAGTGGAATCCATCAGAAC 957
   Drosophila melanogaster polypeptide SEQ ID NO 28023
   Myers EW
  Ş
  ABB67077 standard; protein; 345
   PWD,
  23-MAR-2001; 2001WO-US009231.
   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
  entry)
   New isolated nucleic acid
genes from Drosophila and
interactions.
   ጛ
  Drosophila melanogaster
  Venter JC, Adams M,
  (first
  WPI; 2001-656860/75.
N-PSDB; ABL11180.
  CORP
  WO200171042-A2
   26-MAR-2002
   27-SEP-2001
   )
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  101
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   GCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTG 126
   127 CGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACA 186
   246
   294
   354
  137
   411
  531
   196
  591
  651
  711
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175, and the encoded proteins (ABBL30773-ABR2072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
  60 HisGluAlaValLysSerGlyIleAsnTyrIleAspThrAlaProTrpTyrGlyGlnGly
   |||::::::
|138 AspVallleGlnIleHisAspIleGluPheAlaLysAspLeuAspIleVallleAsnGlu
   ATTGTGGCTACTAAGTGTGGTAGATATAAA------GAAGGTTTTGATTTTCAGT
   GCTGAGAGAGAAAGAGTATTGACGAGAGCTTGGAGGCTTCAGCTTGATTATGTT
   GACATACTTCATTGCCATGACATTGAGTTCGGG----TCTCTTGATCAGATTGTGAGTGAA
  ACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACT
  GGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGAT
  GTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCT
  ThrasnaladiyProGlnProTrpHisProAlaSerAspGluGlnLysAlaIleAlaArg
   AAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGGTTAGCGCCGTTGGTTTTGGT
  TACTTGAAGAGCAAAGGTGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTT
   345
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99
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
   (1-345)
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124 GTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGA 183
   ACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGAC 243
  :::||| ::: |||:::|||:::
ThrAlaAlaLysAlaArgGluSerValLysArgSerLeuGluLeuLeuGlnLeuAspArg 138
   ACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTC 528
   ||||
ThrAlaTyrAspValAspValLeuLysGluCysAlaGluArg---GlyLysGlyArg1le 197
  GATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTA 588
   CITACAGAACAAGGICCICCIGAAIGGCACCCIGCIICCCCIGAGCICAAGICIGCAAGC 708
  AAAGCCGCAGTTGCTCACTGCAAATCAAAGGCAAGAAGATCACAAAGTTAGCTCTGCAA 768
  ||||
LysArgGlyAlaGluIleCysGlnLysArgAsnValGluLeuGlyLysLeuAlaMetTyr 277
  CTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTA-----AAGAATCTGACATGGCCAAGT 942
  TACATTGTGGCTACTAGTGTGGTAGATATAAA------GAAGGTTTTGATTTC 291
  ::: ||| ::: ||| 41 GlyAlaThrLeuSerLyBLeuPheSerAspAspPheAspArgGluGluGlyIleLeuThr
   81 GlyLysSerGluGluLeuLeuGlyGlnAlaLeuLys-----AspValProArgGluAla
   |||| :::||||||||||
TyrTyrIleAlaThrLysValAlaArgTyrdluLeuAspProAsnAsnMetPheAspTyr
  292 AGTGCTGAGAGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTAT
  ||||::
|LeuSerAsnAlaGlyProGlnSerTrpHisProGlySerProGluLeuLeuAlaValGly
   67 GCCTCCGCTCGGAAGTGTCTTCGGT----CCAGTCGCCGAAGATGATGCCGTCGCCACC
  GTTGACATACTTCATTGCCATGACATTGAGTTCGGG---TCTCTTGATCAGATTGTGAGT
  GAAACAATTCCTGCTCTTCAGAAACTGAAACAAAGAGGGGAAGACCCGGTTCATTGGTATC
   CCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCCATTAGCAATGGGCCTC
US-10-606-300-12 (1-960) x ABB71229 (1-342)
   Ž
  protein; 294
   (first entry)
  standard;
   26-MAR-2002
  184
   244
   66
  119
   139
  159
  179
   529
   198
  589
   218
  238
   709
  169
   278
   829
   298
  352
  409
  469
   649
  258
  ABB60118;
   889
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  ABB60118
  RESULT
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  is
   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6176-ABIJ30511), expressed DNA sequences (ABIJ61840-ABIJ6175) and the encoded proteins (ABBSP3737-ABBS72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
::::::::
ThrMetSerGlyLeuProGluValSerThrPheLeuThrGlyMetGlnThrArgGlnLeu
                                     AGTTTAGCAAAC---AAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAG
   Drosophila; developmental biology; cell signalling; insecticide;
   Disclosure; SEQ ID NO 40479; 21pp + Sequence Listing; English.
   342
111
71
111
115
   Drosophila melanogaster polypeptide SEQ ID NO 40479
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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   Myera
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   ABB71229 standard; protein; 342
   PWD,
  23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
   23-MAR-2001; 2001WO-US009231
   63e-49
   544.50
58.75%
36.56%
32.94%
   Ŀ
   Drosophila melanogaster
   Venter JC, Adams M,
  (first
   WPI; 2001-656860/75
   (PEKE ) PE CORP NY
   Similarity:
  |||
Leu 316
  N-PSDB; ABL15332.
  Ë
   CTG 891
   Percent Similarity:
Best Local Similarity
Query Match:
DB:
  WO200171042-A2
   pharmaceutical
  Sequence 342
   Alignment Scores:
  26-MAR-2002
  27-SEP-2001
   316
              257
  297
   889
  ABB71229
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237

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217 648

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us-10-606-300-12.n2p.rag

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831
  411
   471
  472 GGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGAT 531
   591
  |||:::||||:::||| :::
170 ValValLeuAsnTyrAlaArgTyrThrLeuLeuAspAsnThrLeuLeuArgTyrMetLys 189
  651
  209
  712 GCCGCAGTTGCTCACTGCAAATCAAAGGCAAGAAGATCACAAAGTTAGCTCTGCAATAC 771
   249
   772 AGTITAGCAAACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTA
                  GIGATATIGICATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCT
  592 TACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTT
   832 GAAGAAAATGTTGCAGCAGTTACAGAGCTTGAAAGTCTGGGGGATG------GATCAA
295 GCTGAGAGAGTAAGAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTT
  GACATACTTCATTGCCATGACATTGAGTTCGGG---TCTCTTGATCAGATTGTGAGTGAA
  ACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCCGGTTCATTGGTATCACT
   (KIKK ) KIKKOMAN CORP.
(NODA ) ZH NODA SANGYO KAGAKU KENKYUSHO.
   L-fucose dehydrogenase; L-FDH; enzyme
  AAR51284 standard; protein; 329
  92JP-00243372
  92JP-00243372
   (first entry)
  Pseudomonas sp; No.1143
   L-fucose dehydrogenase
   GAAACTCTG 891
  286 Gluvalieu 288
  (revised)
  WPI; 1994-146990/18.
N-PSDB; AAQ62089.
  JP06090765-A.
  11-SEP-1992;
  11-SEP-1992;
   16-OCT-2003
14-DEC-1994
  05-APR-1994.
  412
  AAR51284;
  355
   532
  RESULT 8
   AAR51284
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   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL0140-ABL16175) and the encoded proteins (ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
  246
  67 GCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTG 126
  CGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACA 186
   294
   247 ATTGTGGCTACTAAGTGTGGTAGATAT-------AAAGAAGGTTTTGATTTCAGT 294
:::||||||||||
71 TyrilealaThrLysValalaArgTyrGlyLeuAspProLysAsnMetPheAspTyrSer 90
   99
   40
  47
  28
   New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
  ::::::||| ||| ||||||:::|||||||| |||| ::
ArgMetGluTyrArgGlnLeuGlySerThrGlyLeuHisValSerLysLeuAlalleGly
  -----PhePheAspAspTyrAspArgGluGluGlyIle
   AAAATAGAGCTTCGAGCTTTGGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGT
  CTGTCTGAGAAAATGCTTGGTAAGGGACTAAAAGGCTTTGCAAGTCCCTAGAAGTGACTAC
   Drosophila; developmental biology; cell signalling; insecticide;
  Disclosure; SEQ ID NO 7146; 21pp + Sequence Listing; English.
  294
102
57
101
7
                melanogaster polypeptide SEQ ID NO 7146
  Length:
Matches:
Conservative:
Mismatches:
Indels:
   Gaps:
   US-10-606-300-12 (1-960) x ABB60118 (1-294)
  PWD.
   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
   23-MAR-2001; 2001WO-US009231
   6.37e-36
420.50
52.48
33.66
25.44
  ፤
  Drosophila melanogaster
  Venter JC, Adams M,
   WPI; 2001-656860/75.
N-PSDB; ABL04221.
  (PEKE ) PE CORP NY
   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  Sequence 294 AA;
   WO200171042-A2
  pharmaceutical
  interactions
  Alignment Scores:
   27-SEP-2001
  41
  127
  48
  187
  29
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Genomic DNA from Arthrobacter oxidans F1 was subjected to restriction enzyme analysis and the N-terminal amino acid sequence of L-fucose dehydrogenase determined. A degenerate probe was synthesised based on this amino acid sequence. The probe was used to screen an Arthrobacter CDNA library to isolate a L-fucose dehydro- genase clone. The isolation of such a clone provides a convenient method for produ. of L-fucose dehydrogenase without the need for induction by L-fucose. The probe may be used to evaluate the extent of expression of L-fucose dehydrogenase. The DNA sequence is widely used to assay L-fucose levels. The protein sequence of L-fucose dehydrogenase. (Updated on 25-WAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
         257 TrpAspArgLeuValArgIleAlaAlaIleCysArgAsnHisAspValProLeuProAla
  817 TCTGTCTCACAGGTAGAAAATGTTGCA---GCAGTTACAGAGCTTGAAAGTCTGGGG
  Isolated gene encoding L-fucose dehydrogenase - useful for prodn.
  ATGGATCAAGAAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCT 918
  ::: ||| |||:::|||
LeuTrpAlaGlu---LeuAlaGluAlaArgLeuIleProThrPro 329
  F1; induction; assay.
  Kato
  Disclosure, Page 8, 16pp, English.
  AAR27118 standard; protein; 321
  Sakai T,
  enzyme by genetic engineering
   92EP-00302170
  91JP-00089184
   3.85e-27
339.50
49.06%
30.94%
20.54%
   (TAKI ) TAKARA SHUZO CO LID
   (revised)
(revised)
(first entry)
   Ε.
  Arthrobacter oxidans;
  Arthrobacter oxydans;
   Fucose dehydrogenase.
  Mitta M, Kotani H,
  WPI; 1992-325548/40.
  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  N-PSDB; AAQ28895.
   Sequence 321 AA;
  24-OCT-2003
25-MAR-2003
01-MAR-1993
   13-MAR-1992;
  29-MAR-1991;
  Alignment Scores:
Pred. No.:
   30-SEP-1992
  EP506262-A1
   AAR27118;
   316
   RESULT 9
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                                      8
  236
  82 AGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGT 141
  201
  261
  85 AlaĠiyArgLeuLeuArgProAsnProGluArgArgProSerGlyLeuAspThrAspAsn 104
   310 AAGAGTATTGACGAGAGCTTGGAGAGCTTCAGCTTGATTATGTTGACATACTTCATTGC 369
   CATGACATTGAGTTCGGGTCTCTTGATCAGATTGTGAGAAACAATTCCTGCTCTTCAG 429
   AAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGATATT 489
  |||:::::: |||||||
LysValArgAlaGluGlyValValIysAlaIleGlyIleGlySerMetValSerAspAla 184
   |||
|185 LeuThrArgAla------ValArgGluAlaAspLeuAspLeuIleMetValAlaGly 201
  591
  651
   652 ACAGAACAAGGICCICCI------GAAIGGCACCCIGCIICCCCIGAGCIC 696
   697 AAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAG 756
  |||||||
67 LeuGlyAlaPheLeuGlnThr----LysProArgAspGluPheValValSerThrLys 84
   56
  99
   81
recombinant DNA and the prepn.
  the
  217 AlaCysAlaGluAsnAlaThrGlyIleValAlaAlaSerValPheAsnSerGlyLeuLeu
  142 CTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTGTCTGAGAAAATG
   592 TACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTT
  :::
237 AlaGinSerGluProLysArgAspGlyArgTyrGluTyrGlyGlnLeuProAspGluLeu
   22 GCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCCTCTCCGCTCGGA
   7 AlaAlaAlaAlaGlyLeuAlaIleProAlaLeuGlyTyrGlyAlaAlaAsnValGly
   CTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAG
   -------TATAAAGATTTTGATTTCAGTGTAAGA
   490 TICACITAIGITCITGAICGAGIGCCICCAGGGACIGICGAIGIGAIAIIGICAIACIGI
   550 CATTACGGCGTTAATGATTCGACGTTGCTG-------GATTTACTACCT
  늉
   prodn.
   The L-FDH gene is new and can be used for the recombinant enzyme. (Updated on 16-OCT-2003 to standardise OS field)
  329
103
62
122
48
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
 - а пем
  US-10-606-300-12 (1-960) x AAR51284 (1-329)
  gene
   262 TGTGGTAGA------
                                       Claim 1; Page 5; 6pp; Japanese.
Novel L-fucose dehydrogenase goof L-FDH using a L-FDH vector.
  5.29e-30
366.00
49.25$
30.75$
  Best Local Similarity:
Query Match:
DB:
   Sequence 329 AA;
   Percent Similarity:
   Alignment Scores:
   370
   430
  165
   271
  202
   No.:
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321 99 58 110 53

Length:
Matches:
Conservative:
Mismatches:
Indels:
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Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; heat behinded; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
   Hinkle GJ, Slater SC,
                        Bacterial polypeptide #23187.
   20-FEB-2003; 2003US-00369493
   21-FEB-2002; 2002US-0360039P
02-DEC-2004 (first entry)
   HINKLE G J.
SLATER S C.
   GOLDMAN B S.
  US2003233675-A1.
   CHEN X.
   18-DEC-2003
   Bacteria.
   (CAOY/)
  (GOLD/)
   (HINK/)
  (SLAT/)
   CHEN/)
   Cao Y,
285
   273
   825
  765
   879
  390
  :::||||||| ||| :::||||||::::: |||||| :::
127 GlnArgLeuGlyThrAspArgIleAspIleValTyrIleHisAspProAsp---AspTyr 145
   -----GATTTACTACCTTACTTGAAG 600
  661 GGTCCTCCT------GAATGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCA 705
   CCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGTCTCGGTATCAAC 153
   CTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAGTGTGGTAGATAT 273
  ACCCGGTTCATTGGTATC-----ACTGGTCTTCCGTTAGATATTTTCACTTAT 498
  48
  68
  86
   ThraspValLeuLeuProValLeuGlyPheGlyGlyAlaProlleGlyAsnLeuTyrArg 28
  ||| :::|||||| GlubalayalSerAlaAlatrpGluGlyGlyValArg
   GITCITGAICGAGIGCCICCAGGGACTGICGAIGIGAIATIGICAIACTGICAITACGGC
   -----ThrLeuLeuGluGlnGlyAlaAlaGlnAspLeuLeuProAlaCysLeu
  :::
AlaAsnLeuLeuAlaAspValCysGluSerHisGlyThrThrLeuProAlaAlaAlaLeu
   ACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCCTCTCCGCTCGGAAGTGTCTTCGGT
  TTCTTCGACACCTCCCCGTATTATGGAGGAACACTGTCTGAGAAAATGCTTGGTAAGGGA
  LeuArgProAsnProSerProGlnGlyLysAspThrGluGlyPheAspValProAspAsp
  ------GATTTCAGTGCTGAGAGAGAAAGAGAGTATTGACGAGAGCTTG
  GAGAGGCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGACATTGAGTTCGGGTCT
  391 CTTGATCAGATTGTGAGTGAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAG
   601 AGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAA
   706 AGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTG
   766 CAATACAGTTTTAGCAAACAAGGAGATTTTCGTCGGTGTTGGTTTGGGATGAGCTCTGTCTCA
   CAGGTAGAAGAAAAT-----GTTGCAGCAGTTACAGAGCTTGAAAGTCTGGGGATGGAT
             US-10-606-300-12 (1-960) x AAR27118 (1-321)
  GTTAATGATTCGACGTTGCTG-
  826
  σ
  94
  53
  154
  49
   214
  69
  87
  286
  331
  451
   499
   185
  559
  198
  RESULT 10
   ADS44757
ID ADS4
XX
AC ADS4
XX
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Goldman BS

chen X,

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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant comprised plant but the ecombinant DNA construct and growing the transforming a plant with the recombinant DNA construct is useful for improving plant with the comproved properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, colerance to herbicides, extreme osmotic conditions, pathogens or peress, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modification of carbohydrate, nitrogen or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lighting production or improved galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the printed specification but was obtained in electronic for form part of the printed specification but was obtained in electronic forms.
   New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
  306
100
64
108
12
   format from USPTO at segdata.uspto.gov/sequence.html
   Conservative:
Mismatches:
Indels:
Gaps:
  Length:
Matches:
  Claim 1; SEQ ID NO 23187; 122pp; English.
  6.19e-27
337.50
51.41$
31.35$
20.42$
WPI; 2004-061375/06.
   Percent Similarity:
Best Local Similarity:
   Ä
   Sequence 306
  Alignment Scores:
   Query Match:
DB:
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ADS44757 standard; protein; 306

ADS44757

```
Protein encoded by Prokaryotic essential gene #3168
  Query Match:
  Wang |
258
   597
   SerlleMetMetGlnPheSerLeuPheAspArgArgProGluGluTrpLeuProLeuLeu 186
  657
  261
   198
  259 AAGTGTGGT---AGATATAAAGAAGGT-------TTTGATTTCAGTGCTGAG 300
  301 AGAGTAAGAAGAGTATTGACGAGAGCTTGGAGGCTTCAGCTTGATTATGTTGACATA 360
   361 CTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGATTGTGAGGTGAAACAATTCCT 420
   GCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCT--- 477
  CCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATA 537
  ProAsnvallieLysGluTyrvalLysLysSer----------Asnlleval 166
   ---CCTGAGCTCAAGTCTGCAAGCAAAGCC-----GCAGTTGCTCACTGCAAATCAAAG 738
  GGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAGATTTCGTCG 798
  GIGTIGGITGGGATGAGCICTGTCTCACAGGTAGAAAAATGTTGCAGCA----- 849
   ||||::: ||| ||| ||| 262 ValileThrGlyAlaSerLysileGluGlnLeuArgGluAsnIleGlnAlaAsnAla 281
  24 GlyThr-------GluLyBAsnLysAlaLeuSerIleLeuAspGluAlaIle 38
  95
                                    23
   -----GITACAGAGCTIGAAAGTCTGGGCATGGATCAAGAAACTCTGTCTGAGGTT 900
   :::|||||| ||| ||| 282 ArgArgLeuThrGluGluGluGluIleLy8AlaLeuGlnSerHisThrLy8GlnAspIle 300
                                   4 ArglysLeuGlyThrSerAspLeuAspIleSerGluValGlyLeuGlyCysMetSerLeu
   79 GGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTC
  139 CGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTGTCTGAGAAA
   199 ATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACT
   538 TIGICATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCTTG
   AAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAA
  207 Lys---ProLeuAspGlnAlaSerGluSerMetLysGlnAsnGlyTyrLeuSerTyrSer
                   CGAGCTTTGGGGAACACAGGCTTAAGGTTAGCGCCGTTGGTTTTTGGTGCCTCTCCGCTC
US-10-606-300-12 (1-960) x ADS44757 (1-306)
  protein; 304
   (first entry)
   ABU17641 standard;
  19-JUN-2003
   153
  167
   799
  478
  850
  ABU17641;
  421
   RESULT 11
  ABU17641
ID ABU1
XX AC ABU1
XX I9-J
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
conclude acid; (2) a host cell containing the vector; (3) an isolated
contined acid; (2) a host cell containing the vector; (3) an isolated
contypeptide or its fragment whose expression is inhibited by the antisense
controlleration or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for
configuration or the activity of a gene in an operon required for
configuration or that has an activity against a biological pathway
crequired for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
configuration or the test compound that inhibits proliferation of an
corganism acts; (9) manufacturing an antibiotic; (10) profiling a
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture computed that inhibits proliferation of
compound's activity; (11) a culture computed that inhibits become
confound's activity; (11) a culture computed that inhibits the
confound's activity; (11) a culture computed that inhibits or collection of
compute is overexpressed or underexpressed; (12) determining the extent
confound's or inhibits processed or underexpressed; (12) determining the extent
confound's or inhibits proliferation of an organism. The antisense mucleic acids required
confounds proliferation or solated enabled mucleic acids are useful for
dentifying processed or seadidate molecules for rational
  drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Antisense; prokaryotic essential gene; cell proliferation; drug design.
  Zyskind JW;
Xu HH;
   New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
  ŖŖ
  Ohlsen |
Forsyth |
  304
92
56
109
47
   Conservative:
Mismatches:
Indels:
  Haselbeck R,
Yamamoto R,
  Length:
Matches:
  Claim 25; SEQ ID NO 45565; 1766pp; English
  Malone C,
Carr GJ,
  06-SEP-2001; 2001US-00948993
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
  21-MAR-2002; 2002WO-US009107
  4.53e-26
329.50
48.68%
30.26%
19.93%
   2001US-00815242
   (ELIT-) ELITRA PHARM INC.
  Zamudio C,
Trawick JD,
   2003-029926/02.
  Bacillus anthracis.
  Percent Similarity:
Best Local Similarity:
   N-PSDB; ACA21511
  Sequence 304 AA;
   WO200277183-A2
   21-MAR-2001;
   Alignment Scores:
   03-OCT-2002
  μÜ
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Bacterial polypeptide #4875.
         02-DEC-2004
480
   540
  645
   :::|||||||:::
203 IleLeuThrAspAsnAsnAlaArgLy8------IleGluArgValLy8GluLy8 218
   360
   TyrilelygalaGluValLysGluSerLeuArgArgLeuGlnThrAspTyrIleAspLeu 115
  CTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGATTGTGAGAGAACAATTCCT 420
  TyrGlnLeuHisGly------GlyThrIleGluAspProlleAspGluThrIleGlu 132
   TCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTG-------GATTTA 585
  202
  705
   GGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTC 138
  AAGTGTGGT---AGATATAAAGAA-------GGTTTTTGATTTCAGTGCTGAG 300
  171 GluTyr-------SerLeuLeuAsnArgArgProGluGluTrp 182
   -----AAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAGATT 792
   28
  23
   75
   78
  24 GlyThr------SerGluAlaGluAlaMetArgIleIleAspGluAlaIle
   ||| ||||||||||::: ||| |||::: ||| ArgGlnLeuGlyAenGtSerLeu
   239 IleValGluSerSerLeuThrGlyThrAlaileGlnTyrCysLeuHisAsnAspThrVal
   TCGTCGGTGTTGGGATGAGCTCTGTCTCACAGGTAGAAAATGTTGCAGCAGTT
                                   CGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCCTCTCCGCTC
   CGTCTCGGTATCAACTTCTTCGACACCCCCCGTATTATGGAGGAACACTGTCTGAGAAA
   199 ATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACT
   301 AGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGCCTTCAGCTTGATTATGTTGACATA
   GCTCTTCAGAAACTGAAACAAGAGGGAAGACCCCGGTTCATTGGTATCACTGGTCTTCCG
   Tragatatiticactitatgitcitgatcgagtgcctccagggactgicgatgigatatitg
   CTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCCATTAGCAATGGGC
  183 PheProLeuLeuAsnGluHisGlnIleSerVallleAlaArgGlyProLeuAlaLysGly
  CTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCA
   706 AGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGC--------
10
Gaps:
                 US-10-606-300-12 (1-960) x ABU17641 (1-304)
   ADN22222 standard; protein; 325 AA.
  LysGlnThrGln 282
   853 ACAGAGCTTGAA 864
  4
   79
  139
   59
   259
   9/
  96
  361
   116
   421
   133
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   541
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant such as maize or soybean. The method of producing a transformed plant to such as maize or soybean. The method of producing a transformed plant excembinant DNA construct and growing the transformed plant where the polymucleotide or polypeptide is useful for improving plant with the combinant DNA construct is useful for improving plants with the polymucleotide or polypeptide is useful for improving plants with improved plant properties, e.g. improved cold, heat or accomplication. The recombinant DNA construct is useful for improved plant properties, e.g. improved cold, heat or a drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or persent increased rate of norceased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified sead oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved lighial production of improved algain production of improved algain production of improved algain production or improved galactonmannan compact of the invention. Note: The sequence cate for this patent did not form part of the printed sepecification but was obtained in electronic correct form part of the printed sepecification but was obtained in electronic correct or scope of the invention. Note: The sequence cate for this patent did not correct form part of the printed sepecification but was obtained in electronic correct form part of the printed sequence cate or the printed second sequence cate or the printed second second second second second second second second
  New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; best tolerance; pathogen tolerance; pathogen tolerance; pathogen tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
   325
87
70
120
7
  Goldman BS;
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
  Chen X,
  Claim 1; SEQ ID NO 4875; 122pp; English.
  Slater SC,
  20-FEB-2003; 2003US-00369493
  21-FEB-2002; 2002US-0360039P.
   7.69e-26
327.50
49.22%
27.27%
19.81%
  WPI; 2004-061375/06.
   CHEN X.
GOLDMAN B S.
   HINKLE G J.
SLATER S C.
  Hinkle GJ,
   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  US2003233675-A1.
  Sequence 325 AA;
  Alignment Scores:
  18-DEC-2003
  Bacteria.
   (HINK/)
(SLAT/)
(CHEN/)
(GOLD/)
  (CAOY/)
  Cao Y,
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(first entry)

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Bacterial polypeptide #7635.
02-DEC-2004
390
  495
   276
  159
  219
   612
   840
  296
  -----TATAAAGAA 279
   160 ArgAspGluGlyValValLysAlaVal-----GlyLeuGlyValAsnGluTrpGln 176
   177 ValAlaHisGluAlaIleArgArgGlnAspPheAspCysLeuLeuLeuAlaGlyArgTyr 196
   613 GGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCT--- 669
   GCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCA 780
   41
   61
   -----TrpTyrProArgAspGlnTyrValLeuSerThrLysValGlyArgLeuLeuLys 79
   66
                          99
   21
   436 AAACAAGAGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGATATTTTCACT
   237 AlaLysTyrAsnTyrAlaProAlaProGluAlaileLeuGluArgValArgLysMetGlu
   ::: ||| ::: ||| ::: || || HisProAlaraThrValAlaGlnLeuGluAspAsn
                          CTTAAGGTTAGCGCCGTTGGTTTTGGTGCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTC
  GCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTC
  GACACCTCCCCGTATTATGGAGGAACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAG
  GCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAGTGTGGTAGA------
  GGTTTTGATTTCAGTGCTGAGAGAGAGAAAAGAGTATTGACGAGAGCTTGGAGAGCTTT
   340 CAGCTTGATTATGTTGACATACTTCATTGCCATGACATTGAGTTCGGGTCT-----
   -----CTTGATCAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTG
   TATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTAC
   GGCGTTAATGATTCGACGTTGCTGGAT ---TTACTACCTTACTTGAAGAGCAAAGGTGTG
   ServalileLeuGlyGlyGlyTyrAsnSerdlyIleLeuAlaThrGlyAlaValProGly
   AACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAGAAAT
   GTTGCAGCAGTTACAGAGC-----TTGAAAGTCTGGGGATGATCAGAAA 886
   ::: |||||| :::|||::: 297 -LeuGlnThrPheArgAlaGluIleProAlaGluPheTrpAlaGluLeuLy8Arg 314
        US-10-606-300-12 (1-960) x ADN22222 (1-325)
   ADN24982 standard; protein; 308
   .......
  721
  841
  001
  22
  160
  220
   62
  271
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   496
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a crop plant cauch as maize or soybean. The method of producing a transformed plant to such as maize or soybean. The method of producing a transformed plant cauch as maize or soybean. The method of producing a plant with the carcombinant DNA construct and growing the transformed plant, where the polymucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plants with the companiant DNA construct is useful for improving plants with construct or polypeptide is useful for improving plant properties. Cromerased plant properties, e.g. improved cold, heat or advought tolerance, tolerance to plant disease, better growth rate by modification content, improved plant disease, better growth rate by modification of carbohydrate, introgen or phosphorus use and/or uptake, by modification of forbotosynthesis or by providing improved plant growth and development under at least one stress condition, improved lightin production or improved galactomannan condition, improved lightin production or improved galactomannan condition, improved lightin production or improved galactomannan compact of the invention. Note: The sequence date for this patent did not form part of the printed specification but was obtained in electronic form part of the printed specification but was obtained in electronic
   provide
   New recombinant DNA construct comprising a promoter positioned to provi for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein arbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.
  308
82
65
113
38
  Goldman
   Conservative:
Mismatches:
Indels:
Gaps:
   Matches:
   Claim 1; SEQ ID NO 7635; 122pp; English.
  Chen X,
  Slater SC,
   20-FEB-2003; 2003US-00369493.
   21-FEB-2002; 2002US-0360039P.
  .95e-25
   322.00
49.33%
27.52%
19.48%
  HINKLE G J.
SLATER S C.
CHEN X.
   WPI; 2004-061375/06.
   GOLDMAN B S.
  Hinkle GJ,
  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
   US2003233675-A1.
  18-DEC-2003.
   Bacteria.
  (CHEN/)
  CAOY/)
  (HINK/)
   (SLAT/)
  Cao Y,
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US-10-606-300-12 (1-960) x ABU29907 (1-329)
 229 GTCCCTAGAAGTGACTACATTGTGGCTACTAAGTGTGGTAGA-------270
   289 TTCAGTGCTGAGAGAGAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGAT 348
   349 TATGTTGACATACTTCATTGCCATGACATTGAGTTCGGGTCT---------390
   ::::::|||||||
HisīleAspīleAlaLeuIleHisAspīleAspValPheThrHisGlyGluArgGlnPro 138
  ::: :::
GlualaileArgArgGlnAspPheAspCysLeuLeuLeualaGlyArgTyrThrLeuLeu 195
  196 GluGlnAspAlaLeuAspGlyPheLeuProLeuCysGluLysLysGlnValSerValIle 215
   699
   ::: |||||||
236 ABNTYrAlaProAlaProGluAlaIleLeuGluArgValArgLyBMetGluGlnValCy8 255
   730 AAATCAAAGGCCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAG 789
  AGCGCCGTTGGTTTTGGTGCCTCCGCTCGGAAGTGTCTTCGGTCCCAGTCGCCGAAGAT 108
  CCGTATTATGGAGGAACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAA 228
  -----CTTGATCAGATTGTGAGTGAACAATTCCTGCTCTTCAGAAACTGAAACAAGAG 444
  GATTCGACGTTGCTGGAT----TTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATA 621
  GATGCCGTCGCCACCGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCC 168
                            21 AspSerAlaAlaLeuIleLysAlaAlaTrpAspAlaGlyValArgTyrPheAspThrAla 40
  86
   Antisense; prokaryotic essential gene; cell proliferation; drug design.
   |||||||
59 TyrProArgAapGlnTyrValLeuSerThrLyaValGlyArgLeuLeuLyaProArgArg
   271 -----TATAAAGATTTTGAT
  ::::::
79 ArgAlaGluIleAspPheAlaProTrpValAspGlyLeuProPheGluProValPheAsp
   GGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTT
  GATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAAT
  622 AGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCT------
  790 ATTTCGTCGGTGTTGGGTTGGGATGAGCTCTGTCTCACAGGTAGAAAAATGTT 843
  Protein encoded by Prokaryotic essential gene #15434
US-10-606-300-12 (1-960) x ADN24982 (1-308)
   ABU29907 standard; protein; 329 AA
   (first entry)
  19-JUN-2003
                                    ٦
   41
   119
  265
  691
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screening

New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

invention relates to an isolated nucleic acid comprising any

25; SEQ ID NO 57831; 1766pp; English.

Claim

Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

Haselbeck R, Yamamoto R,

Malone C, Carr GJ,

Zamudio C, Trawick JD,

'nά

Wang

2003-029926/02.

N-PSDB; ACA33777

06-SEP-2001; 2001US-09948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC.

21-MAR-2002; 2002WO-US009107

Enterococcus faecium.

WO200277183-A2.

03-OCT-2002

```
The invention relates to an isolated nucleic acid comprising any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibited by the antisense nucleic acid; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required gene or the gene product lies or a gene on which the test compound that inhibits proliferation of an compound, sactivity; (11) a culture comprise or tell gene product lies overexpressed or underexpressed; (12) determining the extent proliferation of an organism acts; (9) manufacturing an antibicit; (10) profiling compound, sactivity; (11) a culture compound that inhibits steed to which each of the strains is present in a culture or collection of the strains; or (13) identifying to homologous nucleic acids are useful for strains; or (13) identifying the target of a compound that inhibits the confidentifying proliferation in cells other than S. aureus, S. typhimurium, CC dentifying decovery programs, or for screening homologous nucleic acids acids required for proliferation in cells other than S. aureus, S. typhimurium, CC the target prokaryotic essential genes. Note: The sequence data for this parent did not form part of the printed specification, but was obtained for the printed specification.
   323
1104
1124
1246
  Length:
Matches:
Conservative:
Mismatches:
Indels:
  ftp.wipo.int/pub/published_pct_sequences
   3.05e-25
  322.00
49.10%
31.14%
19.48%
   Similarity:
   Sequence 329 AA;
   Percent Similarity:
Best Local Similari
   Query Match:
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29-JUL-2004 (first entry)

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405
  165
  516
  681
   465
   576
   202
   630
   813
   237
   297
   ::: ||||::::::::||| ||| ||| ApgluGlyProTyrGlyGlu 108
   AlaHisArgLysGluIleProPheLeuSerGluGluGluGlnValGlySerThrLeuGluLys 262
   753
  :::|||::: :::|||263 IleLysAlaLeuGlnThrIleAlaVal-------SerArgGlyGlnSerLeuAla 278
   AGCTCTGTCTCACAGGTAGAAGAAAATGTTGCAGCAGTTACAGAGCTTGAAAGTCTGGGG 873
   GCCTCTCCGCTCGGAAGTGTCTTCGGTCCCAGACGAAGATGATGCCGTCGCCACCGTG 126
   CGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACA 186
                   30
   48
  68
  88
99
  ProLeuAlaGlnGlyLeuLeuThrAsnArgTyrLeuHisGlyIleProGluAspSerArg
            |||||||
146 GluGluThrAlaGluAlaLeuMetGlnLeuValArgGlnGlyLysAlaLeuTyrIleGly
  ATCACT------GGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCT
   166 ileSerAsnTyrAsnGlyGluAspThrLysLysMetThrGluIleLeuLysArg-----
   -----CCTGAG
   CTCAAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACA
   AAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGGTTAGCGCCGTTGGTTTTGGT
   ----CTGTCTGAGAAATGCTTGGTAAGGGACTAAAGGCT---TTGCAAGTCCCTAGA
   238 AGTGACTACATTGTGGCTACTAAGTGTGGTAGATATAAAGAAGGTTTTGATTTCAGTGCT
   GATTATGTTGACATACTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGATTGTG
   406 AGTGAAACAATTCCTGCTCTTCAGAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGT
  CCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTG
   CTG-----GATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCT
  CCATTAGCAATGGGCCTCCTTACAGAACAA-----GGTCCTCCTGAATGGCACCCT
   PheSerProGluGluGluLeuArglleAspGlnIleLeuGlu 329
  874 ATGGATCAAGAAACTCTGTCTGAGGTTGAAGCTATTCTCGAG
   GCTTCC------
   517
   67
  31
  127
  49
   187
   69
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ABO77872 standard; protein; 367 AA

AB077872

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polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypetide, for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa attuges for antibacterial drugs, production of P. aeruginosa templates for recombinant production of P. aeruginosa-derived peptides or polypeptides, as target of Pseudomonas species using biochip technology. Sequences or other sequences of Resudomonas species using biochip technology. Sequences AB067826-AB084396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but, was obtained in electronic format from USPTO at
  Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
  174
   234
   91
  115 GTCGCCACCGTGCGCGTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTAT
   |||||||:::
72 AspAlaThrLeuAsnAlaAlaTrpAspAladlyPhcArgTyrTyrAspValSerProHls
   |||||||
92 TyrGlyalaGlyLeuAlaGluGlnArgPheGlyArgLeuLeuSerGly-----LysPro
   GITGGITTITGGIGCCICTCCGCICGGAAGIGICTICGGICCAGICGCGAAGAIGAIGCC
  TATGGAGGAACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCT
  invention relates to Pseudomonas aeruginosa polypeptides and the
  Pseudomonas aeruginosa infection; antibacterial
   AGAAGTGACTACATTGTGGCTACTAAGTGTGGTAGATAT-------
   367
884
60
103
8
  ä
   Length:
Matches:
Conservative:
Mismatches:
Indels:
  Bush
  Disclosure; SEQ ID NO 26618; 455pp; English
  Pseudomonas aeruginosa polypeptide #10047,
  Deloughery C,
  Gaps:
   US-10-606-300-12 (1-960) x ABO77872 (1-367)
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   seqdata.uspto.gov/sequence.html
  98US-0074788P
   99US-00252991
  1.12e-24
  Nolling J,
  317.00
50.17%
29.27%
19.18%
  Pseudomonas aeruginosa
  Bacterial infection;
  WPI; 2003-615309/58.
N-PSDB; ABD11443.
  Best Local Similarity:
Query Match:
DB:
   Sequence 367 AA;
  Rubenfield MJ,
   Percent Similarity:
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   18-FEB-1998;
   27-JUL-1998;
  US6551795-B1
   Alignment Scores:
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||| :::|||:::::||||| |||||| ||||||| ArgAspGluTyrValLeuSerThrLysValGlyArgLeuLeuGlnProAlaSerGlnPro 129
   298 GAGAGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGGCTTCAGCTTGATTATGTTGAC 357
  |||| ::::::: |||||| 190 GlnGlnAlaAlaLeuThrGlnLeuArgAspGluGlyVallle 209
  247 GluAlaLeuAspThrLeuPheProThrCysGlnAlaArgAspValGlyValValGly 266
   CCTGAGCTC-----AAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAG 738
  1111111 ProGlnValAlaGlnArgArgGluGlnLeuLysAlaAlaGluHisCys----- 303
   GGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAGATTTCGTCG 798
  274 -----AAAGAAGGTTTTCAGTGCT 297
  358 ATACTTCATTGCCATGACATT-----GAGTTCGGGTCT------CTT 393
   394 GATCAGATTGTGAGAGAGAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACC 453
  514 CCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTT-----AATGAT 567
  568 TCGACGTTGCTGGATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCT 627
  628 TCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCC 687
  324 ValileProGlyThrAlaAsn 330
  GTGTTGGTTGGGATGAGCTCT 819
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Search completed: November 13, 2005, 08:26:25 Job time : 106 secs

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Aac37387 Arabidops
Acn4814 Cotton pr
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Acn4885 Drosophil
Abl28825 Drosophil
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Acn46035 Cotton pr
Acn38044 Prokaryot
Abl06602 Drosophil
Abl28824 Drosophil
Abl28814 Drosophil
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Ada71938 Rice gene
Acn62765 Cotton ca
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               GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
   4390206 seqs, 2959870667 residues
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Maximum Match 100%
Listing first 45 summaries
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Š. Result

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|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 8 AAAA AAAA AAAAAAAAAAAAAAAAAAAAAAAAAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                                            | A; 960 BP. t.ry)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | e;  <br>  \Quad \Quad                                                                | O-GB001412. B-00007651. TD. er G; 1. 1. dehydrogenase prol in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producing in for producin |
| 911<br>9600<br>1100909<br>110050<br>110050<br>25144<br>9277<br>9277<br>9277<br>9277                                                                                                                                                                                                                                                                                                                                                                                                                                             | 2000<br>650<br>110000<br>273254<br>621<br>993<br>1512                                      | ; cDN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | ehydrogenase<br>romosome 4;<br>haliana.<br>Location/<br>1.960<br>/*tag=<br>/product= | VO-GB<br>3B-00<br>JID.<br>11.<br>71.<br>71.<br>57, 5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                                            | standard<br>01 (fir                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | dehy<br>chrom<br>thal                                                                | 2974-A2.<br>2001.<br>2001; 2001W<br>2000; 2000G<br>ASCORBEX L<br>E N, Wheel<br>31-616482/7<br>AAE11998.<br>Galactose<br>3 the prote<br>3 the prote<br>3 the prote<br>3 the prote<br>3 the prote<br>3 the prote<br>5 Fage 56-5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| "" """ "" "" "" "" "" "" "" "" "" "" ""                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 888<br>89.<br>93.2<br>93.2<br>93.2<br>93.2<br>94                                           | 19526<br>19526;<br>38C-20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | alactos<br>bicide;<br>bidopsi                                                        | OO17: MAR-: MAR-: CO-) rnofi rnofi roor; in 6.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| 122222222222222222222222222222222222222                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 7 8 8 8 9 8 9 8 9 8 9 8 9 9 8 9 9 9 9 9                                                    | 1952<br>PAN<br>PAN<br>18                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | L-g<br>herj<br>Araj<br>CDS                                                           | WO2<br>29-1<br>29-1<br>8 MPI<br>WPI<br>P-PP<br>WOV<br>WOV<br>WOY<br>WOY<br>WOY<br>WOY<br>WOY<br>WOY<br>WOY<br>WOY<br>WOY<br>WOY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| υ υ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | υ υ                                                                                        | RESULT 1 AAD19526 ID AAD5 XX AC AAD5 XX AC AAD5 XX XX AC AAD5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX                                              | \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |

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useful for generating transgenic organisms and modified pants with enhanced ability to synthesise ascorbic acid. L-galDH facilitate the production of a plant that has been genetically modified to express a mutated L-galDH protein which is resistant to herbicides that act against the naturally occurring L-galDH and to identify and/or design compounds that are inhibitors of L-galDH. The compounds can be used, for e.g. in a herbicide which acts on L-galDH and damages or kills plants that express the enzyme. The present sequence is Arabidopsis thaliana L-galactose dehydrogenase (L-galDH) cDNA. The L-galDH gene is located on chromosome 4
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  780
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  840
  9
  TTTGGTGCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGAAGAGTGATGCCGTCGCC
   ACCGIGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGA
  GACTACATTGTGGCTACTAAGTGTGGTAGATATAAAAGAAGGTTTTGATTTCAGTGCTGAG
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  GGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCAAGGAAAGCCGCAGTT
   GCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCA
  AACAAGGAGATTTCGTCGGTGTTGGGATGAGCTCTGTCTCACAGGTAGAAGAAAAT
   1 ATGACGAAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGT
   ATGACGAAAATAGAGCTTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTTAGCGCCGTTGGT
   TYTGGTGCCTCTCCGCTCGGAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCC
  ACCGIGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGA
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  CTTCATTGCCATGACATTCGGGTCTCTTGATCAGATTGTGAAACAATTCCT
   GCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCG
   GCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCG
  TTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTG
  Tracaratricactrarcricarccacrecrecaccaccacrercargicararic
  AGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAA
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  ;
   Length 960;
  Sequence 960 BP; 251 A; 195 C; 251 G; 263 T; 0 U; 0 Other;
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100.0%; Score 960; DB 4; L.
Best Local Similarity 100.0%; Pred. No. 1.2e-304;
Matches 960; Conservative 0; Mismatches 0;
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   61
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The invention relates to generating ascorbic acid or its salt, involves obtaining a recombinant yeast capable of converting an ascorbic acid precursor into ascorbic acid, culturing the recombinant yeast in a medium comprising an ascorbic acid precursor, thus forming ascorbic acid, and soluting the ascorbic acid, and conjusting the ascorbic acid, and isolating the ascorbic acid. Also include are stabilising ascorbic acid or its salt in a medium, by culturing a yeast in a medium comprising a scorbic acid or its salt and a recombinant yeast functionally considered at a recombinant yeast functionally considered from L-galactose dehydrogenase (LODH), L-galactonally carbinono-1, 4-lactone oxidase (ADD), D-arabinose dehydrogenase (ADD) activity, where the recombinant yeast is capable of converting to ascorbic acid at least about 25% ascorbic acid precursor of converting to ascorbic acid at least about 25% ascorbic acid precursor or is capable of producing at least 20 mg ascorbic acid/L medium, when the yeast is cultured in a medium comprising one ascorbic acid precursor. The second produced (Vitamin C) is a powerful antioxidant, a deficiency of which causes scurvy in humans. The present sequence encodes
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                                 960
  ss; gene; ascorbic acid; vitamin C; scurvy; recombinant yeast; L-galactose dehydrogenase; LGDH; L-galactono-1,4-lactone dehydrogenase; AGB; D-arabinose dehydrogenase; ARA; D-arabinono-1,4-lactone oxidase; ALO; L-gulono-1,4-lactone oxidase; GLO; aldonolactonase; AL.
   capable
GAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGTGGAATCCATCAGAACTAA
  Generating ascorbic acid or its salt, involves culturing yeast c converting ascorbic acid precursor into ascorbic acid in medium comprising ascorbic acid precursor, and isolating ascorbic acid.
  A. thaliana cDNA encoding L-galactose dehydrogenase (LGDH)
  U; 0 Other;
  G; 263 T; 0
   Location/Qualifiers
  251
  Claim 14; Page 87; 95pp; English.
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   02-AUG-2001; 2001WO-GB003485
   02-AUG-2000; 2000US-00630983
   (first entry)
   Ø
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K.
  Arabidopsis thaliana.
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P-PSDB; AAU76343.
   Sauer M;
  (BIOP-) BIOPOLO (WHALL) WHALLEY
   WO200210425-A2
   21-MAY-2002
  07-FEB-2002.
   ABK10125;
   Porro D,
  901
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   Key
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.

Arabidopsis thaliana

Arabidopsis thaliana DNA fragment SEQ ID NO: 17196

17-OCT-2000 (first entry)

AAC37387;

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   18-JUN-1999;
18-JUN-1999;
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   14-MAY-1999
   8-MAY-1999
  06-SEP-2000
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AAC37387 standard; DNA; 1221

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| RR 26-MG-1399 9908-0150864P. RR 27-MG-1399 9908-0151065P. RR 27-MG-1399 9908-0151065P. RR 10-120-1399 9908-0151065P. RR 10-120-1399 9908-01513138P. RR 10-120-1399 9908-01513138P. RR 10-120-1399 9908-01513138P. RR 10-120-1399 9908-01513138P. RR 25-138P-1399 9908-01513138P. RR 25-138P-1399 9908-01513138P. RR 25-138P-1399 9908-01513138P. RR 26-138P-1399 9908-01513138P. RR 26-138P-1399 9908-01513138P. RR 26-138P-1399 9908-01513138P. RR 26-138P-1399 9908-01513318P. RR 26-1399 9908-01513318P. RR 27-1399 9908-01508-01508P. RR 27-1399 9908-016089P. RR 27-1399 9908-016089P. RR 27-1399 9908-016089P. RR 26-1399 9908-016089P. RR 27-1299 9908-016089P. RR 26-1299 9908-016089P. RR 26-1299 9908-016089P. RR 26-1299 9908-016089P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1299 9908-0161308P. RR 26-1399 9908- | Query Match         98.6%;         Score 946.4;         DB 3;         Length 1221;           Best Local Similarity         99.8%;         Pred. No. 4.2e-300;         1         Addatum         1;         Indels         1;         Gaps         1;           Qy         1         ATGACGAAATAGAGCTTCGAGCTTTGGGAACACAGGGCTTAAGGTTACGCCGTTGGT         174           Qy         61         TTTGGTGCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCAGGTTAAGGTTAATGTGT         174           Qy         61         TTTGGTGCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCGTCGCTCGC |
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1014
   GAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGTGGGAATCCATCAGAACTAA 1074
  960
   420
   540
  600
  714
  99
  840
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  474
   594
  654
  774
   834
  894
                       414
  GCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCG
  TTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTG
   TCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCTTACTTGAAG
  GCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGGTTAGCTCTGCAATACAGTTTAGCA
  AACAAGGAGATTTCGTCGGGGTTGGGATGAGCTCTGTCTCACAGGTAGAAAT
GACTACATTGTGGCTACTAAGTGTGGTAGATATAAAGAAGGTTTTGATTTCAGTGCTGAG
               GACTACATTGTGGCTACTAAGTGTGGTAGATATAAAGAAGGTTTTGATTTCAGTGCTGAG
   AGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATA
  AGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATA
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   GCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCG
   TTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTG
  TCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCTTACTTGAAG
  AGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAA
  GCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAAGTTAGCTCTGCAATACAGTTTAGCA
  AACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAAAT
  GAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGTGGAATCCATCAGAACTAA
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ACN48774 RESULT

BP ACN48774 standard; cDNA; 564

(first entry) 02-DEC-2004

Cotton primed seed EST Clone ID: LIB3825-027-06-K6-G2, SEQ:3555.

Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety PSF08; library LIB382; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant qrowth; plant yield; plant breeding; tissue printing; se.

Gossypium hirsutum

US2004123340-A1.

24-JUN-2004

12-DEC-2001; 2001US-00021323 

14-DEC-2000; 2000US-0255619P.

The invention relates to 17880 cotton expressed sequence tags (ESTB;
ACNA5220-ACN63099). The ESTB were isolated from CDNA libraries generated
C from primed or non-primed seeds from variety DPS50B, mature seeds from
C variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
C tissue, developing fibres, carpel walls and septa from variety
CC Nucotton3B. The invention also relates to substantially purified
CC invention, and to transformed plants having a nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTB are useful as
CC determine gene function and to determining whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolateing a variety of agronomically significant genes
CC used for isolateing avariety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CI inks in metabolic and catabolic pathways. The nucleic acid molecules are
CS associated with plant growth, quality, yield, and could also serve as
CS inks in metabolic and catabolic pathways. The nucleic acid molecules are
CS during seed germination. The ESTS additionally enable the acquisition of
CS promoters and cis-regulatory elements which will be useful for corporation and cis-regulatory elements which will be useful for corporation to genes. The nucleic acid molecular markers useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein or mRNA and for
CC detecting the expression level or pattern of a protein or mRNA and corporated patence appeasents a specifically claimed BST isolated from a
CC cotton variety DPSOB primed seed coming of a protein or mRNA and corporation or part of the printed specification of the printed specification of the printed seed coming and the printed seed coming and the printed seed coming and the printed seed coming and the printed New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes. segdata.uspto.gov/sequence.html?DocID=US20040123340 Ziegler TB; Claim 1; SEQ ID NO 3555; 34pp; English. Fincher KL, Deikman J, Feng PCC, DEIKMAN J. FENG P C C. FINCHER K L. ZIEGLER T E. WPI; 2004-479808/45. (DEIK/) I (FENG/) I (FINC/) I 

Sequence 564 BP; 156 A; 97 C; 135 G; 175 T; 0 U; 1 Other;

DB 13; Length 564;

62 caaatigrigggagatatcgrgaaggrtrtrgatrtrcagrgcrgagagagraacraaaagcat 121 377 61 AATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTAC TGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGACAT Gaps 4 Indels 0; Mismatches 126; Score 335; DB 1 Pred. No. 5e-99; 34.9%; Matches 434; Conservative Similarity 198 ß 318 Query Match Local a ઠે a ઠે ઠે

rcargaaacciriccaccriccacricarrargricarararrariccarccarcar 181 437 TGAGTTCGGGTCTCTTGATCAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAA 122 182 378 셤 8 셤

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The invention relates to 17880 cotton expressed sequence tags (ESTs; ACM 5220-ANN 5309). The ESTs were isolated from CDM libraries generated from primed or non-primed seeds from variety DB50B, mature seeds from variety Coker 312 Boswell 96 Field, and androectum tissue, gynoecium tissue, develophing fibres, carpel walls and septe from variety Nucotton33B. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid construct as molecular tags to isolate genetic regions, to isolate genes, to map
   480
   540
  420
  677
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  737
557
  New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
  TGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGG
  cerraargarregacerrecregarrracracerracrrgaagacaaaggrerer
   carraarcarreaacarresassarrrarrescerractreaaaaccaaa-srerrescer
  GATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCA
   aarcalericie de la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra del la contra de la contra del la co
   CCCTGCTTCCCCTGAGCTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAA
  recescarerecesasereasererecensecesasereceserererararerasasasas
   Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety DF908; lbrary LIB3825; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; se.
  Cotton primed seed EST Clone ID: LIB3825-027-Q6-N6-G2, SEQ:3629.
   Ziegler TE;
   Claim 1; SEQ ID NO 3629; 34pp; English.
  GGGCAAGAAGATCACAAAGTTAGC 761
  541 AGGAAAGAATATTTCGAAGTTAGC 564
   Fincher KL,
   ВР
   14-DEC-2000; 2000US-0255619P.
   ACN48848 standard; cDNA; 563
  12-DEC-2001; 2001US-00021323
  (first entry)
   Deikman J, Feng PCC,
   (DEIK/) DEIKMAN J.
(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
   WPI; 2004-479808/45.
   Gossypium hirsutum
  to map genes.
  US2004123340-A1
  24-JUN-2004.
  02-DEC-2004
  ACN48848;
   302
  558
   362
   421
   678
   481
   738
   ACM48848/C
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members of a particular gene family. The nucleic acid molecules may be members of a particular gene family. The nucleic acid molecules may be casciated with plant growth, quality, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to mitigate stresses encountered during seed germination. The BSTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express any significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically chemes, genetic and molecular mapping, and in cloning of agronomically catentificant genes. The nucleic acid molecules are further useful for detecting the expression level or pattern of a protein or mRNA and for detecting the presence or quantity of a protein by tissue printing. The present sequence represents a specifically claimed BST isolated from a cotton variety DPSOB primed seed cDNA library (LIBBSES). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
   ö
   640
  504
   700
   444
   760
  384
  324
   880
  TTAAACAGGTTGAAGAGAATGTTGCCGCTGCAACAGAACTTGCATATTCGGAAAGATC 264
  940
   CTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAG
   ATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGGTGTGATAAGTGCTTCTCCATTAGCAA
  TGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCAAGT
  AAGAAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAA
   Gaps
  Drosophila, developmental biology; cell signalling; insecticide
   .;
0
   Drosophila melanogaster genomic polynucleotide SEQ ID NO 13036.
  DB 13; Length 563;
  Sequence 563 BP; 157 A; 126 C; 112 G; 168 T; 0 U; 0 Other;
   Score 224.8; DB 13; Length
Pred. No. 9.5e-63;
0; Mismatches 97; Indels
  segdata.uspto.gov/seguence.html?DocID=US20040123340
   GTGGAATCCATCAGAACTAA 960
   GCGGAATTCAACGAAGCTGA 184
   ВP
  23.4%;
74.5%;
   ABL20521 standard; DNA; 1038
  (first entry)
  Query Match
Best Local Similarity 74.5
Matches 283; Conservative
  pharmaceutical; gene; ds
   Drosophila melanogaster.
   WO200171042-A2
  26-MAR-2002
   581
   ABL20521;
  563
  503
  881
  263
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AAGGCCATTGCCCGGAAGGCATCGGAGGTCTGCAAGGAACGCCGCGCGAGCTGGGCAAG 813
   142 ridgieccacircrecaagererricrecaagerricaaregagagagagagareeraae 201
   123 CGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGG 182
   202 GGTGCAGGAAGCCATTAGATCCGGTATCAACTACATAGACACGGCTCCCTTTTATGGCCA 261
  capable of detecting 1000 or more genes from brosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-ABB27072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
  697 AAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAG
   TGGTGCCTCTCCGCAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCAC
   Gaps
   invention relates to an isolated nucleic acid detection reagent
  developmental biology; cell signalling; insecticide;
  Score 98.2; DB 4; Length 1051;
Pred. No. 6.6e-21;
0; Mismatches 348; Indels 12;
  Drosophila melanogaster genomic polynucleotide SEQ ID NO 37948.
   Sequence 1051 BP; 242 A; 271 C; 305 G; 233 T; 0 U; 0 Other;
  Claim 1; SEQ ID NO 37948; 21pp + Sequence Listing; English.
   Myers EW
  ABL28825 standard; DNA; 1051 BP.
   Li PWD,
  772
  23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
  Match 10.2%;
Local Similarity 49.9%;
les 359; Conservative (
   23-MAR-2001; 2001WO-US009231
   814 creeccareracraca
  TTAGCTCTGCAATACA
  (first entry)
  Drosophila melanogaster.
  pharmaceutical; gene;
   Adams M,
  WPI; 2001-656860/75.
   (PEKE ) PE CORP NY
  WO200171042-A2
  26-MAR-2002
  Drosophila;
  27-SEP-2001
   Venter JC,
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  ABL28825;
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   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   165
   225
   276
   516
   516
   157 GAGGAGGTATTAAAACTGTGCACGAGGCCGTAAAGTCAGGCATCAACTACATTGACACT 216
   397 GGCCTGGACTACGTTGATGTCATCCAGATTCACGATATCGAGTTCGCCAAGGATCTGGAC 456
   CAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGG 456
  CCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTG 576
  574 GCCGGAAGACTCGATACGGTCCTCACCTATGCCAGATACACCCTGACCGATGAAACGCTC 633
  CTGGATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTA 636
  637 GCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTC 696
  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
   217 GCTCCCTGGTATGGTCAGGGTCGCTCTGAGGAGGTCCTGGGGACTGGCCCTAAAAGGATGTG
  cceceggaarccracrararceccacgaagreecrcecracgaacregacracgaraaa
   106 GATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACC
   TCCCCGTATTATGGAGGAACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTG
   C-----AGTCCCTAGAAGTGACTACATTGTGGCTACTAAGTGTGGTAGATATAAAGAA
   GGTTTTGATTTCAGTGCTGAGAGAGAGAAAAAGAGTATTGACGAGAGCTTGGAGAGGCTT
   CAGCTTGATTATGTTGACATACTTCATTGCCATGACATTGAGTTCG----GGTCTCTTGAT
   457 ATTGTGATCAACGAGACACTGCCCACTTTGGAGCAGCTGGTCAAGGAGGAGGCAAGA
   TTCATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCT
   ricarriccaererecerracecearricegreerraggaerrecreaececa---aca
  cregagiacciegariricircaagreceagaacciegegegerearereecedagerear
   Gaps
  12;
  11.5%; Score 110; DB 4; Length 1038; 50.9%; Pred. No. 8.5e-25; ive 0; Mismatches 320; Indels 1:
  Sequence 1038 BP; 263 A; 257 C; 304 G; 214 T; 0 U; 0 Other;
  Claim 1; SEQ ID NO 13036; 21pp + Sequence Listing; English.
  Myers EW
  PWD,
  23-MAR-2001; 2001WO-US009231
   2000US-0191637P
2000US-00614150
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   Matches 344; Conservative
  Venter JC, Adams M,
   Query Match
Best Local Similarity
   WPI; 2001-656860/75.
  CORP NY
   23-MAR-2000;
11-JUL-2000;
    27-SEP-2001
  (PEKE ) PE
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   226
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  GATATIGICATACTGICATTACGCCGTTAATGATTCGACGTTGCTGGATTTACTACCTTA 593
   GGTGCTCAACTATGCCCGCTACACCCTGTTGGACAACACTTTGCTGCTGCGCCACATGAAGGC 678
   crirccassasareseceresecrirererereresececesecarereresearreteras 738
  739 CAACGCTGGACCCCAGTCCTGGCATCCTGGTAGTCCGGAACTCCTAGCTGTGGCGAAACG 798
   CGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACA 772
  AGGCAAATCGGAAGAGCTGCTTGGCCAGGCGCTCAAGGATGTGCCCCGGGAGGCCTATTA
   TGCCAAGGCTCGGGAGAGTGTGAAGCGTAGTCTGGAGCTGCTCCAGTTGGACAGGGTGGA
AACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGC-----AAGTCCCTAGA
   AGTGACTACATTGTGGCTACTAAGTGTGGTAGATATAAAGAAGGT-TTTGATTTCAGTGC
  322 TATAGCAACTAAAGTTGCACGTTACGAGTTGGATCCAAACAATATGTTCGACTATACGGC
   TGAGAGAGTAAGAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGA
   CATACTTCATTGCCATGACATTGAGTTCGGGTC---TCTTGATCAGATTGTGAGTGAAAC
   ceraciacacerrcardacercearecececercerericades
  AATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGG
  caracccircicoaddagaracerccaddcddaaaaddcrcdarrcarcdagaricacdc
  474 TCTTCCGTTAGAIATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGT
  CTACGATGTGGACGTGCTGAAGGAGTGTGCCGAGCG----GGGCAAAGGTCGCATCCAGGT
  Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety DPSOB; library LiBBR25; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
  Cotton primed seed EST Clone ID: LIB3825-012-Q1-K6-C6, SEQ:2292
   Fincher KL, Ziegler TE;
   BP
   ACN47511 standard; cDNA; 570
  12-DEC-2001; 2001US-00021323
  14-DEC-2000; 2000US-0255619P
  (first entry)
   Feng PCC,
  DEIKMAN J.
FENG P C C.
FINCHER K L.
ZIEGLER T E.
  Gossypium hirsutum
  US2004123340-A1.
   24-JUN-2004.
  02-DEC-2004
   Deikman J,
   714
                           262
   297
   382
   357
  442
   414
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The invention relates to 17880 cotton expressed sequence tags (ESTS;
ACM45220-ACM63099). The ESTS were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DPSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoccium
variety Coker 122 Boswell 96 Field, and androecium tissue, gynoccium
comprimed or their fragments encoded by nucleic acid molecules of the
Invention, and to transformed plants having a nucleic acid construct
comprising a nucleic acid of the invention. The cotton ESTS are useful
molecular tags to isolate genetic regions, to isolate genes are
molecular tags to isolate genetic regions, to isolate genes where
comprising a nucleic acid of the invention. The cotton ESTS are useful
molecular tags to isolate genetic regions, to isolate genes are
molecular tags and electron and to determining whether genes are
molecular tags to isolate genetic regions, to isolate genes are
languages of particular gene family. The nucleic acid molecules may be
used for isolating a variety of agronomically significant genes important in initiating and maintaining
seed germination. The ESTS additionally enable the acquisition of
commons and cis-regulatory elements which will be useful to express
agronomically significant genes in these tissues and/or other tissues,
and also permits the acquisition of molecules are further useful for
cetecting the expression level or pattern of a protein or maken
cotton variety DESOB primed seed cDNA library (LIBBASE). The esquence represents a specifically claimed EST isolated from a
cotton variety DESOB primed seed cDNA library (LIBBASE). The sequence of
cetecting the presence or quantity of a protein or maken
cotton variety DESOB primed seed cDNA library (LIBBASE). The sequence of
cetecting the presence or quantity of a protein or maken
cotton variety DESOB primed seed cDNA library (LIBBASE).

The sequence of the sequestion level or pattern of a protein or maken
cotton variety professor.

The cotton variety of a protein by tissu
   320
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   64
  solated nucleic acid molecule that encodes a plant protein or its ent, useful for isolating a variety of agronomically significant associated with plant growth, quality or yield, and as molecular
   ccaaactagaaargagaccrcrcggaaacacgggccraaagcrcagragcgrcgcrrcg
  GTGCCTCTCCGCAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCG
  GAGCTTCTCCTCGGCAGCGTCTTCGGTTCCGTTTCCGAAAGCGACGCTGTCGCCTCCG
   CGAAAATAGAGCTTTCGAGCTTTGGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTG
  Gaps
   Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety DF908; library LIB385; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
   Cotton primed seed EST Clone ID: LIB3825-013-Q1-K6-E6, SEQ:2400.
  ;
0
  DB 13; Length 570;
   TGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATT
  TCCTCGAAACCTTCCGCCTCTGAATCAACTTCTTCGACACCTCTTCGTAAT
   Sequence 570 BP; 147 A; 152 C; 96 G; 172 T; 0 U; 3 Other;
  47; Indels
  Score 95.8; DB 13
Pred. No. 2.8e-20;
0; Mismatches 47
  SEQ ID NO 2292; 34pp; English
  BP
   10.0%;
  ACN47619 standard; cDNA; 484
   (first entry)
   Matches 124; Conservative
2004-479808/45.
   Local Similarity
   02-DEC-2004
  isolated
  ACN47619;
  ß
  261
   65
   321
  125
  381
   Claim 1;
   Query Match
   RESULT 9
  ACN47619
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The invention relates to 17880 cotton expressed sequence tags (BSTB;

ACM45220-ACM63099). The ESTS were isolated from CDNA libraries generated
from primed or non-primed seeds from variety DPSOB, mature seeds from
cvariety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septe from variety
CC from primed or tansformed seeds from variety
Nucotton33B. The invention also relates to substantially purified:
CC fivention, and to transformed plants having a nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTS are useful as
CC determine gene function and to determining whether genes are
members of a particular gene family. The nucleic acid molecules may be
CC used for isolate genetic regions, to isolate genes
CC used for isolating a variety of agronomically significant genes
CC used for isolating a variety of agronomically significant genes
CC also useful for identifying genes important in initiating and molecules are
CC also useful for identifying genes important in initiating and maintaining
CC also useful for identifying genes important in initiating and maintaining
CC gene germination or that may be used to mitigate stresses encountered
during seed germination. The ESTS additionally enable the acquisition of
CC during seed germination. The ESTS additionally enable the acquisition of
CC promomically significant genes in these tissues and/or other tissues
CC commomically significant genes in these tissues and or serves
CC detecting the expression level or pattern of a protein or servence
CC detecting the presence or quantity of a protein by tissue printing. The
CC detecting the presence or quantity of a protein or protein or protein or protein or protein or protein or protein or present sequence represents a specifically claimed Stream of the printed seed claimed in electronic format dinedection the printed sequence or quantity of a protein or protein or p
   New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
   segdata.uspto.gov/seguence.html?DocID=US20040123340
   Ziegler TE;
  Claim 1; SEQ ID NO 2400; 34pp; English.
   Fincher KL,
  12-DEC-2001; 2001US-00021323.
   14-DEC-2000; 2000US-0255619P
  (DEIK/) DEIKMAN J.
(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
   Deikman J, Feng PCC,
   WPI; 2004-479808/45.
                      Gossypium hirsutum.
   tags to map genes.
   US2004123340-A1.
   24-JUN-2004.
   (DEIK/)
(PENG/)
```

20 GAGCTTTGGGGAACACAGGGCTTAAGGTTTAGCGCCGTTGGTTTTGGTGCCTCTCCGCTCG 79 Gaps .. 0 9.3%; Score 89; DB 13; Length 484; 3.9%; Pred. No. 4.4e-18; ve 0; Mismatches 40; Indels Sequence 484 BP; 128 A; 121 C; 93 G; 142 T; 0 U; 0 Other; 40; 73.98; Best Local Similarity 73.9 Matches 113; Conservative Query Match

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355 GGCTCGGAATCAACTTCTTCGACACCTCTACGT 387
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Bb ACN46035 standard; cDNA; 575 ACN46035; 

02-DEC-2004 (first entry)

Cotton primed seed EST Clone ID: LIB3825-013-Q1-N6-E6, SEQ:816.

Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety DE908; library LIB3825; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.

Gossypium hirsutum.

US2004123340-A1.

24-JUN-2004.

12-DEC-2001; 2001US-00021323.

14-DEC-2000; 2000US-0255619P

(DEIK/) DEIKMAN J. (FENG/) FENG P C C. (FINC/) FINCHER K L. (ZIEG/) ZIEGLER T E.

Ziegler TE; Fincher KL, Deikman J, Feng PCC,

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 816; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (ESTB;
ACN45220-ACN63099). The ESTB were isolated from cDNA libraries generated
from primed or non-primed seeds from variety DBSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
c variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
c variety Coker 312 Boswell 96 Field, and septa from variety
C Nucotton3B. The invention also relates to substantially purified
c proteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a nucleic acid construct
C comprising a nucleic acid of the invention. The cotton ESTB are useful as
molecular tags to isolate genetic regions, to isolate genes, to map
c members of a particular gene family. The nucleic acid molecules may be
C genes, to determine gene family. The nucleic acid molecules may be
C used for isolating a variety of agronomically significant genes
c associated with plant growth, quality, yield, and could also serve as
c links in metabolic and catabolic pathways. The nucleic acid molecules are
also useful for identifying genes important in initiating and maintaining
c seed germination or that may be used to mitigate stresses encountered
c used germination or that may be used to mitigate stresses encountered
c promoters and cis-regulatory elements which will be useful to express
c advances in genes. The nucleic acid molecular markers useful for
detecting the expression level or pattern of a protein or mRNA and for
c detecting the expression level or pattern of a protein or mRNA and for
c detecting the expression level or pattern of a protein or mRNA and for
c detecting the presence or quantity of a protein by tissue printing. The
c present sequence represents a specifically claimed EST isolated from a
c cotton variety DBSOB primed seed cDNA library (LIBB3825). The sequence

Gaps

9

Indels

342

378

498

579 555 639 615 669 675

```
343 CITCALTATGITGACATACTTCATTGCCATGACATTGAGTTCGGGTC---TCTTGATCAG 399
   460 ATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCA 519
   TCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTA 759
  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
   319 TIGGACAGGGIGGACATACTACAGGTTCATGACGTGGACGCGGCACCCAATCTAGACATA
  259 TTTGACTATTCGGCTGACAAAGCTCGGGAGGGTGTGAAGCGGAGTCTGGAGCGGCTCCAG
   379 GIGCIGAAIGAGACCAIACCCTCTCGAGGAGTACGTCCAGGCGGGAAAGGCTCGATTC
   cécaric - - - addiderecica acratecricéria caccirra ada ca acacerridore
   640 ATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCAAG
  rriegia circi rica ga a a consea e con con contro con contro de con
  TITGATITICAGIGCIGAGAGAGAAAGAAAGATATIGACGAGAGCTIGGAGAGGCITCAG
   400 ATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTC
  520 GGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTG
   580 GATITTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCA
   developmental biology; cell signalling; insecticide;
  Drosophila melanogaster genomic polynucleotide SEQ ID NO 13033
ed. No. 5e-15;
Mismatches 238;
   Myers EW
50.5%; Pred. No.
                   0
   BP.
   PWD,
   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
   standard; DNA; 3724
  23-MAR-2001; 2001WO-US009231
   GCCATGTACTATA 748
   (first entry)
   ŗ
                          Conservative
  pharmaceutical; gene; ds
   Drosophila melanogaster
  GCTCTGCAATACA
   Adams M,
   WPI; 2001-656860/75.
  (PEKE ) PE CORP NY.
Best Local Similarity
  WO200171042-A2
   26-MAR-2002
  Drosophila;
   27-SEP-2001.
   Venter JC,
                          249;
   499
  556
  919
   ABL20520
   439
  700
  260
  ABL20520
                       Matches
  RESULT 12
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  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell indevelopmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6176-ABIJ6511), expressed DNA aequences (ABIJ6175) and the encoded proteins (ABBS7137 ABBS72072). The sequence data for this patent did not form part of printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   ö
   946
  298
  886
    at
  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
   CICTGICTGAGGTIGAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGTGGAA
  AGGITIGAAGAGAATGITIGCCGCTGCAACAGAACTIGTACTGTTCGGGAAAGATCATGAAA
   crcraecreaedresaaccaarccreaaeccaereaadaarcaeacareecceaaa
   Gaps
  the US patent office
  Drosophila melanogaster expressed polynucleotide SEQ ID NO 14291
   developmental biology; cell signalling; insecticide;
   ö
  Length 575;
   8.4%; Score 80.2; DB 4; Length 885;
  Claim 1; SEQ ID NO 14291; 21pp + Sequence Listing; English.
  885 BP; 205 A; 225 C; 264 G; 191 T; 0 U; 0 Other;
   Seguence 575 BP; 187 A; 121 C; 99 G; 168 T; 0 U; 0 Other;
   Indels
                     seqdata.uspto.gov/sequence.html?DocID=US20040123340
   Query Match 8.5%; Score 81.2; DB 13;
Best Local Similarity 75.4%; Pred. No. 1.8e-15;
Matches 101; Conservative 0; Mismatches 33;
    format directly from
   Myers EW;
   BP.
   PWD,
  23-MAR-2001; 2001WO-US009231.
   23-MAR-2000; 2000US-0191637P.
   ABL06603 standard; cDNA; 885
  TCCATCAGAACTAA 960
   TTCAACAAAGCTGA 284
    obtained in electronic
   (first entry)
   ŗ
   pharmaceutical; gene; ss
   Drosophila melanogaster.
   Adams M,
  WPI; 2001-656860/75.
  (PEKE ) PE CORP NY
  P-PSDB; ABB62500
  WO200171042-A2
   26-MAR-2002
   27-SEP-2001
   Venter JC,
   Sequence
  417
   887
  357
  947
   297
  ABL06603
  Query Match
   RESULT 11
ABL06603
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263 GTGGTAGAT 271
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  2271
   2211
   2151
                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA aequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
  2390 GAGGAGGGTATTAAAACTGTGCACGAGGCCGTAAAGTCAGGCATCAACTACATTGACACT 2331
  2150 GGCCTGGACTACGTTGATGTCATCCAGATATCACGATATCGAGTTCGCCAAGGATCTGGAC 2091
  225
  279
   339
  2090 ATTGTGATCAACGAGACACTGCCCACTTTGGAGCAGCTGGTCAAGGAGGGCAAGGCAAGA 2031
  340 CAGCITGAITAIGITGACATACTICATIGCCATGACATTGAGITCG---GGICTCTIGAT 396
   397 CAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGG 456
   106 GATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACC
  166 TCCCCGTATTATGGAGGAACACTGTCTGAGAAAATGCTTGGTAAGGGGACTAAAGGCTTTG
  C----AAGTCCCTAGAAGTGACTACATTGTGGCTACTAAGTGTGGTAGGATATAAAGAA
   2270 CCGCGGGAATCCTACTATATCGCCACGAAAGTGGCTCGCTACGAACTGGACTACGATAAA
   280 GGTTTTGATTTCAGTGCTGAGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTT
   2210 ATGTTTGACTTTAGTGCCAAGAAGACGCGCGAAAGCGTGGAGAAGAGCTTGAAACTACTT
   Gaps
  6
   prokaryotic essential gene; cell proliferation;
  Query Match 7.4%; Score 71.2; DB 4; Length 3724; Best Local Similarity 52.8%; Pred. No. 1.1e-11; Matches 204; Conservative 0; Mismatches 173; Indels 9;
  Sequence 3724 BP; 985 A; 815 C; 802 G; 1122 T; 0 U; 0 Other;
             Claim 1; SEQ ID NO 13033; 21pp + Sequence Listing; English.
   2030 ricarideagigrececriracecear 2005
   482
  TTCATTGGTATCACTGGTCTTCCGTT
   Prokaryotic essential gene #19701
   21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
   21-MAR-2002; 2002WO-US009107.
   ACA38044 standard; DNA; 984
   (first entry)
  Mycobacterium avium.
  gene.
   dB;
  WO200277183-A2
  design;
   19-JUN-2003
  03-OCT-2002
   Antisense;
  226
  457
   ACA38044;
  drug
  RESULT 13
   ACA38044

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ACA3

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ACA3

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Prok

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Arug

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Arug

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Myccc

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Myccc

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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) an bost cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits a phological pathway required for proliferation, or that thas an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a gene required for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism. The antisense nucleic acids are useful for to which each of the strains is present in a culture or collection of strains proliferation of an organism. The antisense nucleic acids are useful for form form proliferation in cells other changes are useful for cultured for proliferation in cells other than S. sureus, S. typhimurium, K. pneumonlasor P. seruginosa. The present sequence data for this patent did correct format directly form MIPO at compound the contract of the princed specification, but was obtained in cells other expenses and contract of contract of the princed specification. The sequence data for this patent did contract of the princed specification of the princed specification of the princed specification of the princ
  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
  74 Greacresescentecceaceaceacecececearcaccargarceceaececececece 133
  TCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTGTCTGAGAAAATGC 202
  134 rodogarcaacrictrogacaccoccadcadracoccricososocorcroaacoccrido 193
  TTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAGT 262
  194 rasiscalas recentares de la contra de la recenta de la resida de la resida de la recentarion de la residad de la recentaria del recentaria de la recentaria de la recentaria del recentaria del recentaria de la recentaria de la recentaria de la recentaria de la recentaria de la recentaria de la recentaria de la recentaria de la recentaria del recentaria de la recentaria del recentaria de la recentaria de la recentaria de la recentaria de la recentaria de la recentaria de la recentaria de la recentaria del recentaria de la recentaria del recentaria del recentaria del recentaria de la recentaria de la recentaria del recentaria d
   14 carricoscaladaceceserros de destrator de controlo de carricolo de la car
  GTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGTC
  Zyskind Jw;
Xu HH;
   Gapa
   ö
  Length 984;
   Sequence 984 BP; 160 A; 325 C; 346 G; 153 T; 0 U; 0 Other;
   Ouery Match 7.1%; Score 68.2; DB 8; Length 9
Best Local Similarity 54.6%; Pred. No. 4.8e-11;
Matches 136; Conservative 0; Mismatches 113; Indels
   Ohlsen KL,
Forsyth RA,
  Haselbeck R,
Yamamoto R,
  Claim 14; SEQ ID NO 25914; 1766pp; English
  ftp.wipo.int/pub/published_pct_sequences
   Malone C,
Carr GJ,
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
   Malone
   (ELIT-) ELITRA PHARM
  Zamudio C,
Trawick JD,
  WPI; 2003-029926/02.
P-PSDB; ABU34174.
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2107 GGTGCAGGAAGCCATTAGATCCGGTATCAACTACATAGACACGGCTCCCTTTTATGGCCA 2048
  63 TOGIGCCITCICCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCAC 122
   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
   New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                            1280 GCTCACTCATTGGGACTCTTGAGAAACGCTGGACCACATGCATCGCATCCCGGTAGTCA
   123 CGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGG
630 TCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCC
   690 TGAGCTCAAGTCTGCAAGCCAAAAGCCGCAGTTGCTCACTGCAAAATCAAAGGGCAAGAAGAT
  1220 GGAAATCCTGGCCGTGGCCAAACGGGGGCCGAAATCTGCCAGCAGGAACGTGGAGCT
  2167 redrieceacitereceaagererreredangaerregaregedagagageareereae
   developmental biology; cell signalling; insecticide;
   ..
  melanogaster genomic polynucleotide SEQ ID NO 37945.
   Length 3308;
  Sequence 3308 BP; 898 A; 727 C; 732 G; 951 T; 0 U; 0 Other;
  Claim 1; SEQ ID NO 37945; 21pp + Sequence Listing; English.
   0; Mismatches 138; Indels
   Score 56.2; DB 4;
Pred. No. 8.8e-07;
   Myers EW;
   1160 GGGAAAGCTGGCCATGTACTATA 1138
  750 CACAAAGTTAGCTCTGCAATACA 772
   BP
   PWD,
   ABL28824 standard; DNA; 3308
  23-MAR-2001; 2001WO-US009231.
   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
   Query Match
Best Local Similarity 53.4%;
Matches 165; Conservative
  (first entry)
   ፰
  pharmaceutical; gene; ds
   Drosophila melanogaster.
   Adams M,
   WPI; 2001-656860/75.
  (PEKE ) PE CORP NY.
   WO200171042-A2.
  26-MAR-2002
  27-SEP-2001.
   Drosophila;
   Venter JC,
  Drosophila
  ABL28824;
  RESULT 15
ABL28824/
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   1458
  1457 GGCTCGATTCATCGGAGTCACCGCCTACGATGTGGACGTGCTGAAGGAGTGTGCCGAGCG 1398
   1397 GGGCAAGGGTCGCA---TTCAGGTGGTGCTCAACTATGCTCGTTACACCTTTTAGACAA 1341
  1340 CACCTTGCTGCGCTACATGAAGAACTTCCAGAAAATGGGAGTGGGCGTTGTCTGTGCGGC 1281
   449
  509
   18
  629
   510 AGTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTC 569
  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABIJ6176, ABIJ30511), expressed DNA sequences (ABIJ61775) and the encoded proteins (ABBS70777-ABBJ2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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  APPLICANT: Forro, Danilo
APPLICANT: Sauer, Michael
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  Sequence 3489, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Miegand, Roger C.
   ANTI-SENSE:
FRAGNENT TYPE:
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ORGANISM: Arthrobacter Oxidans
  1013 Accederedescrerces 1031
  DOCUMENT NUMBER:
FILING DATE:
PRILOND DATE:
RELEVANT RESIDUES IN SEQ ID NO:
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INFORMATION FOR SEQ ID NO: 3:
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TYPE: NUCLEIC ACID
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TOPOLOGY: linear
MOLECTULE TYPE: genomic DNA
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OTHER INFORMATION: /n
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CRANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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   US-07-855-793-3
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   VOLUME:
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  Sequence 3, Application US/07855793

Patent No. 521780

GENERAL INFORMATION:
APPLICANT: MESANOTI MITTA et al.
TITLE OF INVENTION: L-PUCOSE DEHYDROGENASE GENE,
TITLE OF INVENTION: L-PUCOSE DEHYDROGENASE BY THE USE OF SAID MICROORGANISM
TITLE OF INVENTION: DEHYDROGENASE BY THE USE OF SAID MICROORGANISM
TITLE OF INVENTION: DEHYDROGENASE BY THE USE OF SAID MICROORGANISM
NUMBER OF SEQUENCES:
ADDRESSES: Wenderoth, Lind & Ponach
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STREET: BOS.
COMPUTER READABLE FORM:
MEDION TYPE: Diskette, 5.25 inch, 500 Kb
OPERATING SYSTEM: MS-DOS
SOFWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/855,793
FILING DATE: 1920133
FILING DATE: 1920134
FILING DATE: 1920134
FILING DATE: 1930134
FILING DATE: 1930134
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US-09-902-540-1166/c

i Sequence 1166, Application US/09902540

i Sequence 1166, Application US/09902540

j Patent No. 6833447

i GENERAL INFORMATION:

j APPLICANT: Goldman, Barry S.

j APPLICANT: Slater, Steven C.

j APPLICANT: Wiegand, Roger C.

j TILLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

j FILE REFERENCE: 38-10(15849)

j CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B CURRENT PAPLICATION NUMBER: US/09/902,540 CURRENT FILING DATE: 2001-07-10 PRIOR PAPLICATION NUMBER: 60/217,883 PRIOR PILING DATE: 2000-07-10 NUMBER OF SEQ ID NOS: 16825 LENGTH: 999
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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Patent No. 6551795

Patent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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TITLE OF INVENTION: AERCHANGAR FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1999-02-18
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PRIOR PLING DATE: 1998-02-18
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NUMBER OF SEQ ID NOS: 33142
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; Sequence 9791, Application US/09252991A
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   ) ORGANISM: Pseudomonas aeruginosa US-09-252-991A-10047
  US-09-252-991A-10047
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  GENERAL INFORMATION:

APPLICANT: Griffais, R.

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT PPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
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PRIOR FILING DATE: 1998-07-27
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US-09-252-991A-9791
  TYPE: DNA ORGANISM: Chlamydia pneumoniae
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463310 recreacececeaacacrearrerrerrirrecrecececeaearcecacraa 463251

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4.0%; Score 38; DB 4; Length 1230230; ilarity 51.1%; Pred. No. 14; Conservative 0; Mismatches 85; Indels 0;

Query Match Best Local Similarity Matches 89; Conserva

TYPE: DNA ORGANISM: Chlamydia pneumoniae

US-09-438-185A-1

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APPLICANT: Stephens, Richard
APPLICANT: Stephens, Raichard
APPLICANT: Mitchell, Wayne
APPLICANT: Kalman, Sue
APPLICANT: Talman, Sue
APPLICANT: The Regents of the University of California
FILE REFERENCE: Oll9941-00041105
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT FILING DATE: 2002-03-13
CURRENT FILING DATE: 1998-11-12
PRIOR PILING DATE: 1998-11-12
PRIOR PILING DATE: 1998-10-08
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; Sequence 1, Application US/09438185A
; Patent No. 6822071
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us-10-606-300-12.rni

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   Sequence 3767, Application US/09902540
Fatent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Misser, Steven C.
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APPLICANT: Misser, Misser, Steven C.
APPLICANT: Misser, 
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US-09-949-016-13465
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ORGANISM: Human
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  US-09-902-540-3767
   US-09-902-540-3767
   Query Match
   3est Local
Matches 6
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  GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: PUTH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 80/99/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,468
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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POTHER INFORMATION:
US-09-596-002-28
  Lagace, Robert, E.
Lagace, Robert, E.
Lagace, Robert, E.
TITLE CANT: BETGE, Kim. L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES O.
FILE REFERENCE: PM-0008-4 US
CURRENT FILING DATE: 2000-6-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR PILING DATE: 1999-06-18
NUMBER OF SEQ ID NO SEQ ID NO SEQ ID NO SEQ ID NO 28
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US-09-949-016-13165/c
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completed: November 13, 2005, 08:07:16
   Job time : 217 secs
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  APPLICANT: LYON DOUGHTE-Stamm et al APPLICANT: LYON DOUGHTE-Stamm et al APPLICANT: LYON DOUGHTE-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: BEDIERRIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TILLE OP INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REPERRNCE: 38-10(15.849)B

CURRENT PELLING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 05/217,883

PRIOR PILING DATE: 2000-07-10

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; Patent No. 6380370
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Local Similarity 57.0%;
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   ; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1183
   Query Match
Best Local S
Matches 65
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RESULT 15 US-09-710-279-3603

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1684 ircaaraaagrcacriaaarcrirrrgagrararrgaacargrrcarcragaaraacrrg 1743
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  464 GTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGA 523
                   Patent NO. 6703492
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
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  Gaрв
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Application US/09710279
  TYPE: DNA ORGANISM: Artificial Sequence
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13219, A 315234, A 315534, A 31553, Ap 28022, Ap 29198, A 221348, A 22400, Ap 2160, Ap 2160, Ap 2165, Ap 28021, Ap

Title: Perfect score:

Sequence:

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TITLE OF INVENTION: Gene Sequence
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CURRENT APPLICATION NUMBER: US/10/240,136A
CURRENT FILING DATE: 2003-07-14
PRIOR PRIJING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 7
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CURRENT FILING DATE: 2003-06-25
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SOFTWARE: Patentin Ver. 2.1
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Publication No. US20050019879A1
GENERAL INFORMATION:
APPLICANT: Porro, Danilo
APPLICANT: Sauer, Michael
TITLE OF INVENTION: Ascorbic Acid Production from Yeast

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Sequence 11457

Sequence 11457

Sequence 11457

Sequence 11457

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

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APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

ITTLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: 10110437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 11457

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; APPLICANT: La Rosa Thomas J
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APPLICANT: Zhou Yihua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
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; CURRENT FILING DATE: 2003-04-28
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   APPLICANT: La Rovalic, David K.
APPLICANT: La Rovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Charles and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
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CURRENT FILING DATE: 2003-04-28
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  ATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCTTACTTGAAGAG 602
   AGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGTGGAATCCATCAGAACTAA 960
   CAAGGAGATTTCGTCGGTGTTGGGTTGAGCTCTGTCTCACAGGTAGAAAATGT
                 581 GTTCGTGGTCGCCACCAAGTGCGCGCTACAGGGAAGGGTTCGACTTCAGCGCCCCG
   CCACTGCCACGACATCGAGTTCACCGACCTCGACCAGATTGTGAGAATGAGACGATTCCGGT
   TCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTT
  GAGCATCTACACTTATGTGCTCGACCAGGTGCCGCCAGGTTCTGTGGATGTGATTCTGTC
   CAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGG
   TCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAA
   AGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATACT
   cércaccecaécerceaceaededecreecacecerceaecracerceaecracerceaecree
   Length 1715;
   DB 21;
  ; OTHER INFORMATION: Clone ID: MRT4577_186846C.1
US-10-425-115-95235
   44.4%; Score 426;
   Sequence 95235, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
   TYPE: DNA
ORGANISM: Zea mays
   RESULT 5
US-10-425-115-95235
   543
  663
  1061
  1121
  843
   903
  1241
   303
   641
   423
  941
  363
  701
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   723
  783
   Query Match
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Sequence 95234, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: About Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 95234
LENGTH: 1295
  61 rereceerreseaacsirriceseaacsiseceeceacaceaceeceeceeceeceeceeceeceecee
   121 ceceiceaciriceaciricairina de la contra del la contra della contra
  241 GTCGCCACCAAGTGCGGCGCCGTACAAGACGAGGGTTTCGACTTCTCCGCCAACCGTGTG 300
  AGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATACTTCAT 366
   CAGAAACTGAAACAAGAGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGAT 486
  181 TCGGAGTCAGTCCTCGGCGATTGCCTCCGCCACGCGGCCGTTCCGCGGGACCGAGTCGTC
  835 daaaicrcgacaaircirgirgaaigaacicircagaacagggggaggaargrggcr
  GCAGTTACAGAGCTTGAAAGTCTGGGGATGGATCAAGAAACTCTGTGTGAGGTTGAAGCT
  TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC
   130 GAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCCCCCGTATTATGGAGGAACACTG
  190 TCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATT
   GTGGCTACTAAGTGTGGTAGATATAAA---GAAGGTTTTGATTTCAGTGCTGAGAGAGTA
   GCTCATGACATCGAGTTCACCCATCTCGAACAGATTGTGAATGAGACAATTCCCGCACTC
                       GAGATTTCGTCGTGTTGGTTTGGGATGAGCTCTGTCTCACAGGTAGAAAAATGTTGCA
   10 ATAGAGCTTCGAGCTTTGGGGAACACAGGCTTAAGGTTAGCGCCCGTTGGTTTTTGGTGCC
  907 ATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGTGGAATCCATCAGAACTAA 960
   DB 21; Length 1295;
   IndelB
  Query Match
40.0%; Score 384.4; DB 21;
Best Local Similarity 64.0%; Pred. No. 3.7e-114;
Matches 630; Conservative 0; Mismatches 321;
  ; OTHER INFORMATION: Clone ID: MRT4577_186845C.1
US-10-425-115-95234
  LOCATION: (1)..(1295)
OTHER INFORMATION: unsure at all n locations
  TYPE: DNA
ORGANISM: Zea mays
   NAME/KEY: unsure
   RESULT 7
US-10-425-115-95234
   847
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   895
   307
   301
  427
  FEATURE:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cabo, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: 18-21(35.53.5) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
SEQ ID NO 13:219
LENGTH: 1434
   ij
   129
  546
   114
  130 GAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCCCCCCGTATTATGGAGGAACACTG 189
  175 CGCGCGCTCGACCTCGGCATCAACTTCTTCGACACCTCCCCGTACTACGGCGGCGGCACGGTC 234
  190 TCTGAGAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATT 249
   AGAAAGAGTATTGACGAGAGCTTGGAGGCTTCAGCTTGATTATGTTGACATACTTCAT 366
  355 ACGCGCAGCATAGACGAGAGCCTCGCCCGGCTGGGGCTGGACTACGTTGACATCCTCCAC 414
  426
  909
   654
  999
  714
   250 GIGGCIACTAAGTGTGGTAGATATAAA---GAAGGTTTTGATTTCAGTGCTGAGAGAGTA 306
   295 GTCGCCCACCAAGTGCCGCTACAAAGACGAGGGTTTCGACTTCCCGCCGACCGTGTG 354
  415 GCCCACGACATCGAGTTCACCCATCTCGACCAGATTGTGAATGAGACAATTCCCGGGCTC 474
   CAGAAACTGAAACAAGAGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGAT 486
   cordana reconoció en recontra de contra   774
  TCCAAATCAAAGGCCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAG 786
   834
   69
  475 CAGAAGATTAAGGAGAGTGGGAAGGCACGTTTCATTGGCATCACCGGGCTGCCCTCAGC
   ATCTACCCTTATGTCCTCGACAGAGAGAGCACCCAGGCTCGATGCTTCTATCTTAC
  70 TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC
  ATTITICACTIVATGITCITGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATAC
  GGTGTTGGGGGTTATCAGTGCTTCGCCACTCCCATGGGTCTTTTAACAGATAATGGGCCA
  10 ATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCC
   55 Arganicicos de contrados de 
  235 TCGGAGTCAGTCCTCGGCGATTGCCTCCGCCACGCGGCCGTTCCGCGGGACCGAGTCGTC
   TGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCTTACTTGAAGAGCAAA
  GGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCT
   ccedadreccaccicacacaacaaciraagicaccarecaegerecaegeardae
   Gaps
   3,
   Length 1434;
   Score 414.8; DB 20; Length
Pred. No. 4.5e-124;
0; Mismatches 327; Indels
   , OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS59142_1
US-10-767-701-13219
   Query Match
Best Local Similarity 65.4%;
Matches 624; Conservative
  ORGANISM: Sorghum bicolor
   307
   367
  535
  547
   667
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  487
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  775
   FEATURE:
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and Other Molecules Associated With
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  574
   CACCAGGCTCGGTGGACGTGATTCTATATTGTCACTACGGGATCAATGACACCTCCC 306
  634
   307 rrerrearcrecreceracricaacacaaccaaccierreccerrarcacrecrecece 366
   694
  rcrccarecercrrraacagaraanegeccaceegagreecaccreecaeaagaac 426
   754
  814
   546
   GCTCTGTCTCACAGGTAGAAAATGTTGCAGCAGTTACAGAGCTTGAAAGTCTGGGGA 874
  909
  934
   ATCAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGGAAGACCC
   TGCTGGATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGGATAAGTGCTTCTCCAT
  TAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGC
   547 ACTCTTTGGAACAGGTGGAGAATGTGGCGCTGCACTGGAGTTGTCAACATCAGGCA
  TGGATCAAGAAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTGACAT
GGCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGACATTGAGTTCGGGTCCTTTG
  GGTTCATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGC
   CTCCAGGGACTGTCGTGTGTTTTGTCATACTGTCATTACGGCGTTAATGATTCGACGT
   TCAAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAA
  NAME/KEY: unsure;

; LOCATION: (1)..(564)

; OTHER INFORMATION: unsure at all n locations

; OTHER INFORMATION: Clone ID: LIB3825-027-Q6-K6-G2

US-10-021-323-3555
  Sequence 3555, Application US/10021323
; Sequence 3555, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
; APPLICANT: Delkman, U111
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.; APPLICANT: Ziegler, Todd E.; TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: NUMBER: US/10/021,323
; CURRENT FILING DATE: 2000-12-12
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
   GGCCAAGTGGAATCCATCAGAACTAA 960
  GGCCTAGCGCCATCCAACAAGCCTGA 692
  TYPE: DNA ORGANISM: Gossypium hirsutum
  367
  667
   127
   187
   515
  247
  575
   635
   427
  755
  487
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   GENERAL INFORMATION.

APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongus
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongus
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 18-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
   ö
   GATCAAGAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGG 936
  275 AAGAAGGTTTTGATTTCAGTGCTGAGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGA 334
  999
  756
   CAGAAGATCAAGGAGAATGGGAAGGCACGGTTCATTGGCATCACCGGGTTGCCTCTCAGC 480
   481 Arciaccerrargicerceacearerageaceaeceaesercesiseacerearerarerare 540
   601 gererregeginarcagiecricececerecaregererraakeaganaaregeeea 660
  969 2-----
  TCTGTCTCACAGGTAGAAAATGTTGCAGCAGTTACAGAGCTTGAAAGTCTGGGGATG 876
  TCTTTGGAACAGGTGGAGGAGAATGTGGCGGCTGCACTGGAGTTGTCAACATCAGGCATC 900
  CTAGCTATGCAGTACAGCTTAATGAACAATGAAATCTCGACAGTTCTTGTTGGAATGAAC
   GGTGTGGGTGTGATAAGTGCTTCTCCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCT
   AAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAG
  ATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATAC
   TGTCATTACGGCGTTAATGATTCGACGTTGCTGCATTTACTACCTTACTTGAAGAGCAAA
   Gaps
   ; 0
   Query Match
35.5%; Score 340.4; DB 19; Length 1134;
Best Local Similarity 68.5%; Pred. No. 8.7e-100;
Matches 470; Conservative 0; Mismatches 216; Indels 0;
CCTGAATGGCACCCTGCTTCCCCTGAGCT------
  ; OTHER INFORMATION: Clone ID: UC-ZMFLB73186H07_FLI
US-10-425-114-31543
  CCAAGTGGAATCCATCAGAACTAA 960
   ccraececarccaacaaccrea 984
   RESULT 8
US-10-425-114-31543
US-10-425-114-31543
; Sequence 31543, Application US/10425114
; Publication No. US20040034888A1
   TYPE: DNA
ORGANISM: Zea mays
   SEQ ID NO 31543
LENGTH: 1134
  667
   697
   817
  841
   106
   607
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  757
   781
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Sequence 28022, Application US/11097143

| Sequence 28022, Application US/11097143
| Publication No. US20050208558A1
| GENERAL INFORMATION:
| APPLICANT: Venter, J. Craig
| TITLE OF INVENTION: ARRAYS, FOR DETECTION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, FOR DETECTION OF 10,000 OR MORE
| TITLE OF INVENTION: ARRAYS, FOR DETECTION OF 10,000 OR MORE
| FILE REFERENCE: 1999-10-05
| PRIOR APPLICATION NUMBER: 60/160,191
| PRIOR PILING DATE: 1999-10-28
| PRIOR PILING DATE: 1999-10-28
| PRIOR PILING DATE: 1999-10-28
| PRIOR PILING DATE: 1999-10-38
| PRIOR APPLICATION NUMBER: 60/164,769
| PRIOR PILING DATE: 2090-01-12
| PRIOR PILING DATE: 2000-01-12
| PRIOR PILING DATE: 2000-01-12
| PRIOR PILING DATE: 2000-01-12
| PRIOR PILING DATE: 2000-01-2
| PRIOR PILING DATE: 2000-01-2
| PRIOR PILING DATE: 2000-01-3
| PRIOR PILING DATE: 2000-01-3
| PRIOR PILING DATE: 2000-01-3
| PRIOR PILING DATE: 2000-01-3
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| PRIOR PILI
  881 AAGAAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAA 940
  263 ATGAAACTCTAGCTGAGGTGGAAGCAATACTGAAGCCAGTGAAGAATCAGACATACTGGCCGA
   563 ATTTATTGCCTTACTTGAAACCAAAGGTGTTGGCGTAATCAGTGCATCTCCACTTGCTA
  503 receactrictracteaerrresticacceaerescarcescarcicescarciceaacricaaer
   CTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAG
  CTCTGCAATACAGTTTAGCAAACAAGAGAGATTTCGTCGGTGTTGGTTTGGGATGAGCTCTG
  106 GATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACC
   Indels 12;
  Length 1038;
  Query Match 11.5%; Score 110; DB 26; Best Local Similarity 50.9%; Pred. No. 2.1e-24; Matches 344; Conservative 0; Mismatches 320;
   GTGGAATCCATCAGAACTAA 960
  203 ecesahrreakesakeersa 184
   , ORGANISM: DROSOPHILA US-11-097-143-28022
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   TYPE: DNA
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  Sequence 3629, Application US/10021323

| Sequence 3629, Application WS/10021323
| Publication No. US20040123340A1
| GENERAL INFORMATION:
| APPLICANT: Delkman, Jill
| APPLICANT: Eng. Feul, Faul C.C.
| APPLICANT: Ziegler, Todd E.
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic No. 10021, 323
| TITLE OF INVENTION: Plants
| FILE REFERENCE: 38-21(52274)B
| CURRENT APPLICANTION NUMBER: US/10/021, 323
| CURRENT PILING DATE: 2001-12-12
| PRIOR FILING DATE: 2001-12-14
| NUMBER OF SEQ ID NOS: 17880
| SEQ ID NO 3629
| LENGTH: 563
  ö
   420
   677
   540
   198 AATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTAC 257
   317
   497
   242 GGAAGCAGGGAAGATTCGTTTCATTGGTATCACCGGGTTGCCCTTGGAATTTTTACTTA 301
  557
   558 CGTTAATGATTCGACGTTGCTGGATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGT 617
   421 AATCAGTGCATCTCCACTTGCTATGGGACTTCTTACTGAGTTTGGTCCACCGGAGTGGCA 480
   678 CCCTGCTTCCCCTGAGCTCAAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAA 737
   61
  498 TGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGG
   362 CATTAATGATTCAACATTGGGGATTTATTGCCTTACTTGAAAACCAAA -GTGTTGGCGT
   TGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGACAT
   378 TGAGTTCGGGTCTTGATCAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAA
   438 ACAAGAGGGGAAGACCCCGGTTCATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTA
   618 GATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCA
   481 TCCGGCATCTCCCGAACTCAAGTCTGCCTGCCAAGCTGCTGCTGTATTGTAAAGAGAA
  Gaps
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  ö
  Length 563
       Length 564;
  Score 224.8; DB 20; Length
Pred. No. 3.9e-62;
0; Mismatches 97; Indels
   Indels
Query Match
34.9%; Score 335; DB 20;
Best Local Similarity 77.0%; Pred. No. 3.3e-98;
Matches 434; Conservative 0; Mismatches 126;
  ; OTHER INFORMATION: Clone ID: LIB3825-027-Q6-N6-G2
US-10-021-323-3629
   738 GGCCAAGAAGATCACAAAGTTAGC 761
   541 AGGAAAGAATATTTCGAAGTTAGC 564
  Query Match 23.4%;
Best Local Similarity 74.5%;
Matches 283; Conservative
   TYPE: DNA ORGANISM: GOSSYpium hirsutum
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US-11-097143-10478

US-11-047143-10478

Publication No. US20050208558A1

GENERAL INPORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DESCOPHILA GENES.

TITLE OF INVENTION: DESCOPHILA GENES.

FILE REFERENCE: CLO00728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-05

PRIOR PLING DATE: 1999-10-19

PRIOR PLING DATE: 1999-10-28

PRIOR PLING DATE: 1999-11-12

PRIOR PLING DATE: 1999-11-12

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR FILING DATE: 1999-12-28

PRIOR PLING DATE: 2000-02-24

PRIOR PLING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PRIOR PLING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PRIOR PLING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008
  48 irringacritrirciccagecenenegacaccarriaracegaaaaccritrccceacress 107
   108 GCTGGACTACCTCGACATGCTTCACGCTCATGACATAGAGTTCACCCATCTCTAACAGAT 167
   TOTGAATGAGACAATTTCCTCTCTCCAAAAGTCCATGGGAACGGGTAGGCACGGCTCAT 227
  TGGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGG 521
  rescarraceserrescrereaaarcracerraresecrreaceserasaces
   63 TEGIGCCTCTCCGCACGAAGTGTCTTCGGTCCCCGAAGATGATGCCCGTCGCCAC 122
   123 CGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGG 182
   202 GGTGCAGGAAGCCATTAGATCCGGTATCAACTACATAGACACGGCTCCCTTTTATGGCCA 261
   183 AACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGC----AAGTCCCTAGA 237
                    TITIGATITICAGIGCIGAGAGAGAAAGAGATATIGACGAGAGCTIGGAGAGCTITA 341
   142 rigirioccaciererecaagererriciecargaerricaargegaggaggericereae
  GCTTGATTATGTTGACATACTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGAT
  TGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCAT
   Length 1051
  522 GACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGA 566
  crneciecececearrerarerricaricaracearecarda 332
   Indels
  Score 98.2; DB 26;
Pred. No. 1.6e-20;
0; Mismatches 348;
  10.2%;
   Query Match
Best Local Similarity 49.9
Matches 359; Conservative
   DROSOPHILA
  US-11-097-143-40478
   ; TYPE: DNA
; ORGANISM: DROSOI
US-11-097-143-40478
   SEQ ID NO 40478
  342
   402
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   462
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   Sequence 29198, Application US/10425115
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Sequence 29198, Application US/2040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con Young K.
APPLICANT: Con Young K.
APPLICANT: APPLICATION NUCLEIC Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
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   **Sequence 2292, Application US/10021323

**Sequence 2292, Application US/10021323

**Publication No. US20040123340A1

**GENERAL INFORMATION:

**APPLICANT: Deikman, Jill

**APPLICANT: Peng, Paul C.C.

**APPLICANT: Pincher, Karen L.

**APPLICANT: Pincher, Karen L.

**APPLICANT: Pincher, Karen L.

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**APPLICANT: Pincher, Karen L.

**APPLICANT: Pincher, Karen L.

**APPLICANT: Pincher, Modeler: US/10/021,323

**CURRENT APPLICATION NUMBER: US 60/255, 619

**PRIOR APPLICATION NUMBER: US 60/255, 619

**PRIOR PILING DATE: 2000-12-14

**NUMBER OF SEQ ID NOS: 17880

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; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Soreen, Serven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Tabaska, Jack E
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
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| AY106400<br>CK284947<br>CV430394<br>CV430394<br>BISS0114<br>BUSS949<br>BUSS949<br>CK297749<br>BX835470<br>CK29749<br>BX835470<br>CK291957<br>BX835410<br>CK291957<br>BISS1318<br>BG64660<br>CK291957<br>BISS1318<br>BG6460<br>CK291957<br>BC660<br>CK291957<br>BC7291957<br>CK291957<br>CK291957<br>CK291957<br>BC7291957<br>CK291957<br>CK291958                                                                                                                                            | ALIGNMENTS  894 bp thaliana Adult cDNA clone GSI 248 (thale cress) ntae; Streptopl liophyta; eudil liophyta; eudil N., Jaillon, O., Quetier, F., &                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | weissenba comparison to Evaluate stional de S comparison comparison stional de S comparison division of division of division of division of division of division of comparinct rried out se construct cried ou | y).  w.genoscope.cns.fr/cster.w.genoscope.cns.fr/cgi-b. Location/Qualifiers l894 /organism="Arabidopsis t' /mol_type="mRNA" /ecctype="Col-0" /db_xref="taxon:3702" /clone="GSLTLSSSESD9" /tissue type="Adult vege /clone_lib="Arabidopsis Col-0"                                             |
| 128<br>128<br>147<br>1735<br>177<br>177<br>178<br>178<br>178<br>178<br>178<br>178<br>178<br>178                                                                                                                                                                                                                                                                                                                                                                                              | BX839165 BX839165 Axabidopsis thaliana cDNA Axabidopsis thaliana cDNA BX839165 BX839165.1 GI:42533248 BXR39165.1 GI:42533248 BXR3700psis thaliana (tha Axabidopsis thaliana (tha Axabidopsis thaliana Eukaryota, Viridiplantee; Spermatophyta; Magnollophroside; euroside II; Bras I (bases I to 894) I (bases I to 894) Gastelli, V., Aury, J.M., J. Gastelli, V., Aury, J.M., J. Menard, M., Cruaud, C., Que                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Caboche, M  Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( Approach ( | .genoscope<br>ocation/qua<br>.genoscope<br>ocation/qua<br>.genoscope<br>organism=""<br>mol type=""<br>mol xref=""<br>db xref=""<br>clone="GSL"<br>tissue type<br>clone_lib="                                                                                                                 |
| 425.6<br>44.5<br>422.2<br>44.2<br>422.2<br>41.0<br>41.0<br>41.0<br>41.0<br>41.0<br>41.0<br>41.0<br>41.0                                                                                                                                                                                                                                                                                                                                                                                      | BX839165 BX839165 BX839165 BX839165 BX839165.1 BX839165.1 BYRBYOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOTOT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | Temple, G., Whole Genon Whole Genon A Combined Annotation Unpublisher Contact: Genoscope Genoscope Genoscope The Sequentife Technicife Sequences) http://www.genoscope.cns.fr/cg http://www.genoscope.cns.fr/cg Location/Qualifiers 1894 Aorganism="Arabidopsi/mol_type="mRNA"   cotype="Col-0"   cotype="Col-0"   clone="GSLTLSS82B09"   tissue_type="Adult v   clone="CSLTLSS82B09"   clone="CSLTLSS82B09"   clone="CSLTLSS82B09" |
| C C C C C C C C C C C C C C C C C C C                                                                                                                                                                                                                                                                                                                                                                                                                                                        | RESULT 1 BX839165 LOCUS DEFINITION ACCESSION VERSION VERSION VERYWORDS SOURCE ORGANISM REFERENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TITLE<br>JOURNAL<br>COMMENT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | FEATURES<br>BOUTCE                                                                                                                                                                                                                                                                           |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 28 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ზ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ជ .                                                                                                                                                                                                                                                                                          |

```
Fax: 81-298-36-9060
Enail: meski@ttc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.
   Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales; Brassicaceae, Arabidopsis.

    (Dases 1 to 638)

   Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
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  249 gactacatricrescractracrescracatatraagaacerriscatricacrescrass
   AGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCCTTCAGCTTGATTATGTTGACATA 360
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   1 ATGACGAAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGT
   Large scale analysis of Arabidopsis full-length cDNA (2002b) Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsiukua, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
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Arabidopsis thaliana
  Location/Qualifiers
GI:19867971
  al Similarity 99.4%; 626; Conservative 0
   309
  61
  129
   181
  189
   241
   Query Match
Best Local S
  301
VERSION
KEYWORDS
SOURCE
ORGANISM
  TITLE
JOURNAL
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   154 CACCGGGGGGGGGTTTCCGGCTATCAGGTATCAACTTCTTCGACACCTCCCCGTATTATGG 213
  333
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   753
  TGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGC 779
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   AAACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAAA 839
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   recrerreadadacreaaacdadadadadadccederrearregrareacregrerrec
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Gaps

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AV825911 RAFL7 Arabidopsis thaliana cDNA clone RAFL07-17-C15 5', RRNA sequence.

DEFINITION

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   Solanum tuberosum (potato)
Solanum tuberosum
Solanum tuberosum
Solanum tuberosum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 998)
Buell, C.R., Hart, A., Ziemann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Ohpublished (2003)
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  846 AGCTGCCCTAGAACTAGAAACGGCTGGAATGGATGAAGAAACATTATCAGAGATCACAGA 905
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  246 CATTCTGTCTACAAAATCTGGGAGGTACAAAGAGGGATTTGATTTTAGTGCTGAGAGGACT
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  546 TIGICACTACAGTGTCAACGATTCAACTTTGGAGGATCTGTTGCCATACCTGAAGAGACAA
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  Contact: Robin Buell
The Institute for Genomic Research
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DEFINITION
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   Solanum tuberosum (potato)

Solanum tuberosum

Solanum tuberosum

Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.

E 1 (bases 1 to 953)

S Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of EGTs from potato callus tissue

L Unpublished (2003)

L Ontate: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-arrayætigr.org

Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/

locata.

Locatan/Qualifiers
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  ö
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Matches 701; Conservative
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CK253464
LOCUS
DEFINITION
  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
   REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
  FEATURES
   ORIGIN
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860 845 920 905

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CK250147 987 bp mRNA linear EST 30-JUL-2004 EST733784 potato callus cDNA library, normalized and full-length Solanum tuberosum cDNA clone POCEDB0 5' end, mRNA sequence. CK250147
   Solanum tuberosum (potato)
Solanum tuberosum solanum tuberosum tuberosum
Solanum tuberosum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
1 (Bases I to 987)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
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Contact: Robin Buell
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  126 GCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAAC 185
  The Institute for Genomic Research 9712 Medical Center Dr. Rockville, MD 20850, USA 9712 Medical Center Dr. Rockville, MD 20850, USA Email: potato-arrayeligr.org Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/ . Seq primer: ATT TAG GTG ACA CTA TAG.
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981 CATTCTGGAACC 992
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  425
   500
   620
  201 cceseaagcriricecricescricarririringacacriccecrarrangeagaae 260
  TCAGAAACTGAAACAAGAGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGA 485
   621 rigicaciacierereacearicaacirireaegasearcieriecearacereaegas 680
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   65
  Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
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Location/Qualifiers
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9712 Medical Center Dr, Rockville, MD 20850, USA
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supplier: RNA was isolated from Nicotiana benthamiana
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (5 C 3 hr, 6hr), and pathogen
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Fseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Reudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."
                  Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, US.
Email: potato-array@tigr.org
Clones can be requested from the University of Institute via http://genome.arizona.edu/orders/
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   CK282536

BST745258 Nicotiana benthamiana mixed tissue cDNA library, normalized, full-length Nicotiana benthamiana cDNA clone NBMAD20 5' cK282536

CK282536
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  Nicotiana benthamiana
Nicotiana benthamiana
Nicotiana benthamiana
Nicotiana benthamiana
Nicotiana benthamiana
Sukaryota, Viridiplantea, Streptophyta; Embryophyta; Tracheophyta;
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asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 979)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
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Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
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REFERENCE AUTHORS

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936 bp mRNA linear EST 30-JUL-2004 EST740883 potato callus cDNA library, normalized and full-length CKZ57246 mRNA sequence. CKZ57246.1 GI:39814226
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1 (bases 1 to 936)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from potato callus tissue
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Solanum tuberosum
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Solanum tuberosum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum.
I (bases I to 948)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTS from potato callus tissue
Other ESTS: EST727503
Contact: Robin Buell
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   880 cdatatritcarcceracracrededardaaaarcerraaadaderedadaaaaararade 939
  65
   The Institute for Genomic Research 9712 Medical Center Dr, Rockville, MD 20850, USA Email: poteato-array@tigr.org Clones can be requested from the University of Arizona Genomics Institute via http://genome.arizona.edu/orders/. Seq primer: ATT TAG GTG ACA CTA TAG.
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Solanum tuberosum (botato)
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Spermatophyta; Magnoliophyta; eudicotyledons;
Spermatophyta; Zismann,V., Karamycheva,S.A. and Baker,B.
Spermation of ESTS from potato callus tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Email: potato-arrayedry. core
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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  126 GCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAAC 185
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Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of An
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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supplier: RNA was isolated from Nicotiana benthamiana
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cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (5 C 3 hr, 6hr), and sthongen
santhomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
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  125
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  TCAGAAACTGAAACAAGAGGGGAAGACCCCGGTTCATTGGTATCACTGGTCTTCCGTTAGA
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Clones can be requested from the University of Arizona Institute via http://ganome.arizona.edu/orders/ . Seq primer: ATT TAG GTG ACA CTA TAG. Location/Qualifiers
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1 (bases 1, to 883)

Stankawicz, Harty, Zismann, V., Karamycheva, S.A., Day, B., Stankawicz, B., Jin, H. and Baker, B.
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   The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
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Contact: Robin Buell
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BST749163 Nicotiana benthamiana mixed tissue cDNA library,
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tissues that include callus, roots from liquid culture
grown plants, heat-excessed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
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BST747208 Nicotiana benthamiana mixed tissue cDNA library,
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end, mRNA sequence.

CK284486

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Stalanta, Harty, Zismann, V., Karamycheva, S.A., Day, B., Staskawicz, B., Jin, H. and Baker, B.
GGGTGTGGGGAGTGATCAGTGCTTCCCCTTTGCAATGGGTCTTCTTACTGAGGCTGGAGC
   Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
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                The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
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  CK282535

SGT 02-AUG-2004

EST745557 Nicotiana benthamiana mixed tissue cDNA library,
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CK282535
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Nicotiana benthamiana
Nicotiana benthamiana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Buelli,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of Ext sequences from Nicotiana benthamiana
Unpublished (2003)
  867
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  Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: TTTTTTTTTTTTTTTTTTTN
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Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
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Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85
Tel: 520 624 595
Fax: 520 621 1559
Email: http://genome.arizona.edu
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

REFERENCE AUTHORS

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Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
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E 1 (bases 1 to 859)
Staskamicz, B., Jin, H. and Baker, B.
Staskamicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr. Rockville, MD 20850, USA
Email: potato-array@tigr.org
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
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Patent No. 6551795

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: ASRUGATIOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30076
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302.50
46.63
28.83
18.30
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  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  LENGTH: 341
  562
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   279
  Pred. No.:
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LeuSerThrLysValGlyArglleLeuThrAlaAlaAspAlaProProLysLeuLeu 109
  GGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCA--- 519
  70 TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC 129
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   GTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATT 462
  |||||||::: ||||::: |||| SerGludrgArgPhedlyArgPheLeuHisThrArgAspAla-----AsnGluTyrVal 89
  10 ATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCC 69
  GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Greeory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10/15849)B
CURRENT APPLICATION NUMBER: 20/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
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  347
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19.03%
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   TYPE: PRT
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RESULT 5
US-09-902-540-10805
; Sequence 10805, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Goldman, Reger C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof; FILE REFERENCE: 38-10(15849)B
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 05/217,883
; PRIOR FILING DATE: 2000-07-10
; RIOR FILING DATE: 2000-07-10
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   654
  714
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271 LeuGluLysLeuAlaAlaAlaArgGlyLeuProProAlaGlnLeuAlaLeuAlaTrpLeu 290
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   103 ThriysAlaPhePheProMetSerAspArgProAsnAlaCysGly------
   GTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATT
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   694 CTCAAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACA
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300.50
46.57%
28.96%
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TYPES: PRT
CORGANISM: Myxococcus xanthus
US-09-902-540-10805
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Best Local Similarity:
Query Match:
DB:
SEQ ID NO 10805
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Pred. No.:
   127
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  S-09-107-532A-553A
Sequence 6891, Application US/09107532A
Sequence 6891, Application US/09107532A
Setent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
AGCTCTGTCTCACAGGTAGAAAATGTTGCAGCAGTTACAGAGCTTGAAAGTCTGGGG 873
   |||| :::|||||| :::||||||| |||| SerArgProGluGlnValHisAspAsnValLysAlaAla-------GlyValLys 301
   è.
   918
   874 ATGGATCAAGAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCT
   332
88
63
132
37
  CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
  US-10-606-300-12 (1-960) x US-09-107-532A-6891 (1-332)
   Matches:
Conservative:
Mismatches:
Indels:
   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
  NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...332
SEQUENCE DESCRIPTION: SEQ ID NO: 6891:
  ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REPERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
  Length:
  ORGANISM: Enterococcus faecium
   MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
   OPERATING SYSTEM: <Unknown>
   LENGTH: 332 amino acids
   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6891:
SEQUENCE CHARACTERISTICS:
  CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
   1.07e-23
296.50
47.19%
27.50%
17.94%
   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
   COMPUTER READABLE FORM
   TYPE: amino acid
  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
   -09-107-532A-6891
  US-09-107-532A-6891
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   FEATURE
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72

GAGCTTCGAGCTTTGGGGAACACAGGCCTTAAGGTTAGCGCCCGTTGGTTTTGGTGCCTCT

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Sequence 6079, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
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309 AsnValGlnAlaLeu---AspLeuHisLeuSerAsnGluAspTyrGlnThrIleAspGlu 327
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  67 GCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTG 126
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  391 CTTGATCAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAAGAGGGGAAG 450
   451 ACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGA 510
  511 GTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCG 570
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185 SerLeuLeuThrArgGluPheGluGlnThrHisLeuGlnThrIleArgGluLeuGlyIle 204
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US-09-328-352-6079
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6079
LENGTH: 334
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296.00
44.93%
26.96%
17.91%
   Percent Similarity:
Best Local Similarity:
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DB:
  Alignment Scores: Pred. No.:
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Sequence 3126, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DELICATION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DELICATION NUMBER: US/09/134,001C
TITLE OF INVENTION: DATE: 1998-08-13
FILE REPREMENCE: GTC-007
FILE NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674

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20 SerGlyIleGluIleSerGluLeuGlyLeuGlyCysMetSerLeuGlyThrAspTyr---
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Mismatches:
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Gaps:
  TYPE: PRT
ORGANISM: Staphylococcus epidermidis
  916 CCTGTAAAGAATCTG 930
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291.50
49.84%
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Best Local Similarity:
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  LENGTH: 314
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DB:
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  235 AGAAGTGACTACATTGTGGCTACTAAG-----TGTGGTAGATATAAAGAAGGT 282
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  Sequence 4, Application US/09673198

Sequence 4, Application US/09673198

Patent No. 6806076

GENERAL INFORMATION:

APPLICANT: MIYAEY, Koichiro; HASHIMOTO, Shinichi; MOTOYAMA Hiroaki;

APPLICANT: MIYAEY, Akio; SETO, Haruo; KUZAYAMA, Tomohisa; TAKAHASHI, Shunji

TITLE OF INVENTION: A process for producing isoprenoid compounds by

TITLE OF INVENTION: antibiotic or weeding activity

TITLE OF INVENTION: antibiotic or weeding activity

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/673,198

CURRENT FILING DATE: 1998-04-14

PRIOR PLILNG DATE: 1998-04-14

PRIOR PLILNG DATE: 1999-02-15

NUMBER: JPS9/035739

PRIOR PLILNG DATE: 1999-02-15

NUMBER: APPLICATION NUMBER: JPS9/035739

PRIOR PLILNG DATE: 1999-02-15

NUMBER: PatentIN VET. 2.0

SEQ ID NO 4

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LENGTH: 348

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  .:::::
LeuAlaArgGlyProValPheLysGlyLeuLeuThrSerLysSerValAspValIleAsp 225
   ::: ||| |||| |||| GluLysPheLysAsnGlyValLeuAspTyr----ThrGlnAspGluLeuGlySer--- 242
   106 AGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTG 765
  :::||| |||:::
-----ThrIleAlaSerIleLysGluLeuGluSerAsnLeuThrAlaLeuSerPhe 259
   GTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGC 558
   654
   -----GAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCA 705
   CAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTAT
  619 ATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACA---------
  886 ACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGG 936
  297 -----IleLygSerAlaArgAsnArgValLygAspIleGluTyr 309
   348
94
60
135
  Length:
Matches:
Conservative:
Mismatches:
Indels:
  4.44e-23
291.00
46.53%
28.40%
17.60%
  ORGANISM: Escherichia coli
   Best Local Similarity:
Query Match:
  Percent Similarity:
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Pred. No.:
   499
  559
   655
   226
  280
                             133
   439
   151
  186
   243
  991
  TYPE: PRT
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----ACACTGTCTGAGAAATGCTTGGTAAGGGACTA 216
   724 CACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGGTCTGCAATACAGTTTAGCAAAC 783
305 -----GluAlaArgGlyGlnLy8LeuSerGlnMetAlaLeuAlaTrpValLeuArgGlu 322
  323 GluLysValThrSerValLeuIleGlyAlaSerLysThrAlaGlnLeuAspAsp---- 340
   GCCACCGTGCGCGAGGCTTTCCGGTCTCGACTTCTTCGACACCTCCCCGTATTAT 177
                  999
  667 CCTGAATGGCACCCTGCTTCCCCTGAG---CTCAAGTCTGCAAGCCAAAGCCGCAGTTGCT 723
   304
  784 AAGGAGATTTCGTCGGTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAAATGTT 843
   ||||||
341 ---AlaValGlyMetLeuGlnAsnArgHisPheThrThrGluGluCysAlaAla1leAsp 359
   67 GCC---TCTCCGCTCGGAAGTGTC-----TTCGGTCCAGTCGCCGAAGATGATGCCGTC 117
  30
   99
   ::: ::: :::||||||| ::: |||||||| ServallleLeuAgpAlaPhaAgGlyValPheHisPheAspValAlaAsnHi9Tyr
AGCAAAGGTGTGGGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAA
  -----GGTCCT
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  267 TyrLeuAsnGlyIleProAlaAspSerArgAlaAlaSerSerArgPheLeuGlnPro
   APPLICANT: Glenn, Matthew
APPLICANT: Lubbers, Mark W
APPLICANT: Lubbers, Mark W
APPLICANT: Lubbers, Mark W
APPLICANT: Lubbers, James
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: them, and methods for using them.
TITLE OF INVENTION: them, and methods for using them.
CURRENT APPLICATION NUMBER: US/09/724,623
CURRENT FILING DATE: 2000-11-28
SUTRENT FILING DATE: 2000-11-28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 86
   334
96
74
107
70
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  US-10-606-300-12 (1-960) x US-09-724-623-86 (1-334)
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Matches:
  Indels:
   ; Sequence 86, Application US/09724623; Patent No. 6476209; GENERAL INFORMATION:
   LENGTH: 334
TYPE: PRT:
7 ORGANISM: Lactobacillus rhamnosus
US-09-724-623-86
   1.52e-21
277.00
48.99%
27.67%
   GGAGGA-----
   GCTATTCTC 912
   360 AlaileLeu 362
  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  Alignment Scores:
  RESULT 11
US-09-724-623-86
   287
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  Pred. No.:
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  APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
ENG DI NO 12541
  ||||||| :::|||:::
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| ||||||| :::|||:::
  GGA------GGAACACTGTCTGAGAAATGCTTGGTAAGGGACTAAAGGCTTTGCAA 228
  :::||| ||| ::: |||:::::||||||| |||
LeuProTyrArgAspGluLeuIleIleSerThrLysAlaGlyTyrThrMetTrpAspGly 139
  394 GATCAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACC 453
  TCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCTTACTTGAAG 600
  TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC 129
   GAG-------GCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTAT 177
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  80
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   ATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCC 69
   217 AsnAspLeuGlyThrProCysllelleHisGlnProArg------Tyr
  :::
81 GlnMetLeuLeuHisAlaPheAspLeuGlyIleThrHisPheAspLeuAlaAsnAsnTyr
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197 LeuTyrValGlyIleSerAsnTyrProLeuAlaGlnAlaArgGluAlaValLygIleLeu
  ---GATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTATTG
   GTCCCT---AGAAGTGACTACATTGTGGCTACTAAGTGTGGGTAGATATAAAGAAGGTTTT
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98
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Matches:
Conservative:
Mismatches:
Indels:
   454 CGGTTCATTGGTATCACTGGTCTTCCGTTA----
             Sequence 12541, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:
  ORGANISM: Klebsiella pneumoniae
   1.4e-21
277.50
49.27%
28.57%
16.79%
  Percent Similarity:
Best Local Similarity:
  ; ORGANISM: Klebsie
US-09-489-039A-12541
 US-09-489-039A-12541
   Alignment Scores:
Pred. No.:
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  484
   541
   231
  TYPE: PRT
   Query Match:
DB:
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GAGGCTTTCCGTCTCCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTG 189
   TCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATT 249
  90 valalarhriysrhrPhePheProTrpArgAsnSerProAsnThrdlyPhe---LeuSer 108
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146 MetGluAlaLeuH1BABDValValLyBAlaGlyLyBAlaArgTyrIleGlyAlaSerSer 165
   -----GTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCC-----ACCGTGCGC 129
   415 ATTCCTGCTCTTCAGAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGT 474
   166 MetGluAlaTrpArgPheAlaLysMetGlnHisThrAlaGluArg-----AsnGlyTrp 183
  184 ThrArgPheileThrMetGlnProGlnTyr-------AsnLeuLeuTyrArg 198
   235 ArgArgThrGlnAsnAspAlaPheAlaLeuLysMetTyrGluAsnAlaAlaLeuLeuAsp 254
   745 AAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAGATTTCGTCGGTGTTG 804
  295 GCTGAGAGAGTAAGAAAGAGTATTGACGAGGCCTTGGAGAGGCTTCAGTTATGTT
::: ::: ::: ::: |||||||||||
   CTTCCGTTAGATATTTTCACT-----TATGTTCTTGATCGAGTGCCTCCAGGGACT
   GTGGCTACTAAGTGT----------GGTAGATATAAAGAAGGTTTTGATTTCAGT
  |||:::
|AspleuPheGln11eHisArgPheAspTyrSerThr------ProValGluGluThr
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  --- CCTGAGCTCAAGTCTGCAAGCCAGCTGCTCCTCACTGCAAATCAAAGGGCAAG
   TTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCCTCCGCTCGGAAGT
  GTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTG----
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Matches:
Conservative:
Mismatches:
Indels:
  TYPE: PRT
ORGANISM: Klebsiella pneumoniae
   3.33e-21
274.00
44.23$
27.75$
16.58$
  Percent Similarity:
Best Local Similarity:
  US-09-489-039A-9552
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 LENGTH: 350
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  71
  250
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  475
   687
  Query Match:
DB:
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  GENERAL INFORMATION:

APPLICANT:
GATY Breton et. al
TITLE OF INVENTION:
NUCLEIC ALD AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION:
NUCLEIC AND THERAPEUTICS
TITLE OF INVENTION:
PREDRANCE:
2709.2004001
CURRENT PEPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE:
2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE:
1999-01-29
NUMBER OF SEQ ID NOS:
14342
SEQ ID NO 9552
  ::: ||| ::: ::: ||| ::: 105 GlulleHisProGlyProTyrGlyValGlyThrSerArgLysAlaVallleGlnGlyLeu 124
   GACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGACATT 378
  379 GAGTICGGGICICITGAICAGAIT---GIGAGIGAAACAAITCCIGCICIICAGAAACIG 435
  251 ThrAsnLysAlaThrPheAlaLysGlyLysGluAlaValValLysGlnLeuAsnAlaLeu 270
  271 AsnGluIleAlaHis-----AspArgAspGlnThrLeuSerGlnMetAlaLeuAlaTrp 288
  AAA------GAAGGTTTTGATTTCAGTGCTGAGAGAGAAAAAAAGAGTATT 318
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  520 GGGACTGTCGATGTGTTGTCATACTGTCATTACGCCGTTAATGATTCGACGTTGCTG 579
   -----GCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATAC 771
  772 AGTTTAGCAAACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTA 831
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   -----GATATTTCACT---TATGTTCTTGATCGAGTGCCTCCA
   |||:: |||| :::::
181 GlualallealaMetPheLysAgpLeuHisThrProPheValLeuAsnGln-----
                           217 AAGGCT---TIGCAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAGTGTGTGGTAATAT
   640 ATGGGCCTCCTTACAGAA-----CAAGGTCCTCCTGAATGG-----CACCCT
  682 GCTTCCCCTGAGCTCAAGTCTGCAAGCAAAGCCGCAGTT---------
  Sequence 9552, Application US/09489039A
Patent No. 6610836
  892 TCTGAGGTTGAAGCTATTCTC 912
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US-09-489-039A-9552
  :::
145 Asp-
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   319
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Sequence 3153.75

Sequence 3153.795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

LENGTH: 358

LENGTH: 358
   203
   259
  534
  651
   204 LeuCysGlnArgAsnGlyValAlaValIleProTrpSerProLeuAlaArgGlyArgLeu 223
   711
   712 GCCGCAGTTGCTCGCAAATCAAAG-----744
  -------AAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCA 780
   781 AACAAGGAGATTTCGTCGGTGTTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAGAAAT 840
   280 IysProGlyValAlaAlaProIleIleGlyProSerArgGlnGluGluLeuAspAspLeu 299
  ::: |||||||
300  LeuGlnAlaVal------AspLeuThrLeuSerProGluGlnIleAspLysLeu 315
::: ||||||:::
----ProlleGluGluThrLeu
  ACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCAAAA
   478 CCGTTAGATATTTTCACTTATGTTCTTGAT---CGAGTGCCTCCAGGGACTGTCGATGTG
  592 TACTTGAAGACCAAAGGTGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTT
  418 CCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTT
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  358
92
60
1133
12
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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   901 GAAGCTATTCTCGAGCCT 918
  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
  GiuAlaProTyrGlnPro 321
   4.27e-20
264.00
46.77%
28.31%
15.97%
   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
   RESULT 14
US-09-252-991A-31535
   US-09-252-991A-31535
   Alignment Scores:
Pred. No.:
   841
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   Sequence 12803, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION
APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREDMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12803
LENGTH: 128
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291 IleGlyAlaThrLysProGluHisLeuSerThrAlaIleSerAlaLeuAspPheSerLeu 310
  GTTGAAGCTATTCTCGAGCCTGTA------AAGAATCTGACATGGCCAAGTGGA 945
  70 TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC 129
   130 GAGGCTTTCCGTCTCCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTG 189
   190 TCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATT 249
   298 GAGAGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGAGCTTCAGCTTGATTATGTŢGAC 357
  -----AlaHisValAlaIleAlaTrpLeuLeuSerLysSerValIleThrAlaProIle 290
  88
   TTGGGGAACACAGGGCTTAAGGTTAGC------GCCGTTGGTTTTGGTGCC 69
   250 GTGGCTACTAAG------TGTGGTAGATATAAAGAAGGTTTTGATTTCAGTGCT
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  328
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133
113
   US-10-606-300-12 (1-960) x US-09-489-039A-12803 (1-328)
  Conservative:
Mismatches:
Indels:
Gaps:
  Length:
Matches:
   ORGANISM: Klebsiella pneumoniae
   6.89e-21
271.00
46.32$
27.91$
16.39$
  ||| ||||||
347 Ile---GlnAsn 349
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Percent Similarity:
Best Local Similarity:
   US-09-489-039A-12803
  US-09-489-039A-12803
  Alignment Scores:
   868
  Query Match:
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  70 TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAA---GATGATGCCGTCGCCACCGTG
   127 CGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACA 186
   187 CTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTAC 246
  GATTTCAGTGCTGAGAGGAGTAAGAAGGTATTGACGAGAGCTTGGAGAGGCTTCAGCTT 345
  GATTATGTTGACATACTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGATT--- 402
   GlyteuSerGluAlaSerAlaGluThrLeuGluArgAla---HisArgValHisPro--- 198
   199 ---IleSerAlaLeuGlnSerGluTyrSerLeuTrpThrArgAspProGluAspThrGly 217
   583 TTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGATAAGTGCTTCTCCATTAGCAATG 642
   834
   523 ACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGAT 582
  GGCCTCCTTACA------GAACAAGGTCCTCCTGAATGGCACCCT 681
  GlyPheLeuThrGlyThrLeuLysArgProGluAspPheAlaAlaAspAspTyrArgArg 257
   -----GAGCTCAAGTCTGCAAGCC 714
  258 PheserproArgPheGlnGlyGluAsnPheAlaLysAsnLeuLysLeuValAspLysVal 277
   715 GCAGTTGCTCACTGCAAATCAAAGGCCAAGAAGATCACAAAGTTAGCTCTGCAATACAGT 774
   ::: ||||||||:::||||| MetGlyMetThrAspPheTyrThrThrGlyGlyAspArgGlnGluAlalleAlaThrLeu 67
   87
  HisArgalavalGluLeuGlyLeuAsnPhePheAspThrAlaAspMetTyrGlyProHis
   10 ATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCC
  GTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGGTTCATT
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US-09-489-039A-9489
; Sequence 9489, Application US/09489039A
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|GluLeuAspAlaile 337
  GAGGTTGAAGCTATT 909
   682 GCTTCCCCT-
   297
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Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFREENCE: 2709.2004.001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
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TITLE OF INVENTION: Ascorbic Acid Production from
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APPLICANT: La Rosa, Thomas J.

APPLICANT: La Rosa, Thomas J.

APPLICANT: Shou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Boukharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Us, 10/10/437,963

CURRENT PILING DATE: 2003-05-14

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i APPLICANT: La Kowalt David K
APPLICANT: Cao Yongwei
i APPLICANT: Cao Yongwei
i APPLICANT: Cao Yongwei
i TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
ITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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CURRENT FILING DATE: 2003-04-28
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| APPLICANT: La Rosa, Thomas J. |
| APPLICANT: APPLICANT: Zhou, Yihua |
| APPLICANT: Cao, Yongwei |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With |
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| APPLICANT: Cao, Yongwal A.
| APPLICANT: Cao, Yongwal A.
| TITLE OF INVENTION: Plants
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| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Plants
| TITLE OF INVENTION: APPLICATION NUMBER: US/10/425,115
| CURRENT APPLICATION NUMBER: US/10/425,115
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US-10-425-115-279897
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Score:
  259 (
  299
               66
   127
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  Sequence 44783, Application US/10767701

Sequence 44783, Application US/10767701

GENERAL INFORMATION:

SENDICANT: Kovalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

SEQ ID NO 44783

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|SerGluSerValLeuGlyAspCysLeuArgHisAlaAlaValProArgAspArgValVal
   907 ATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGTGGAATCCATCAG 954
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32
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Mismatches:
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Best Local Similarity:
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  79
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  FEATURE:
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54.93%
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DB:
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FEATURE:
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  129
   130 GAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCCCCCTATTATGGAGGAACACTG 189
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                                  US-10-606-300-12 (1-960) x US-10-425-115-279897 (1-327)
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Mismatches:
Indels:
Gaps:
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Sequence 69240, Application US/10425114
; Bequence 69240, Application US/0403488A1
; Beducation No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jinddong
; APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; FILE NEWENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69240
; LENTH: 229
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Matches:
Conservative:
Mismatches:
  US-10-606-300-12 (1-960) x US-10-425-114-69240 (1-229)
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Sequence 40479, Application US/11097143

Publication No. US200502085581

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION WILL GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT PILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/150,191

PRIOR PILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-10-28

PRIOR PILING DATE: 1999-110-28

PRIOR PILING DATE: 1999-11-22

PRIOR PILING DATE: 1999-11-22

PRIOR PILING DATE: 1999-11-22
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   472 GGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGAT
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  Sequence 28023, Application US/11097143

Publication No. US20050208558A1

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DREAMS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DREAMS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DREAMS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DREAMS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

FILE REFERENCE: CLOO0728

FRIOR PLILING DATE: 1999-10-05

PRIOR PLILING DATE: 1999-10-19

PRIOR PLILING DATE: 1999-10-12

PRIOR PLILING DATE: 1999-11-12

PRIOR PLILING DATE: 1999-11-12

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PRIOR PLILING DATE: 1999-12-28

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PRIOR PLILING DATE: 2000-02-24

PRIOR PLILING DATE: 2000-02-24

PRIOR PLILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

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NUMBER OF SEQ ID NOS: 43008

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LEAD OF THIRD DATE: 2000-03-23

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APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILLE OF INVENTION: DROSOPHILA GENES.
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 05/157,832
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/150,932
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR PILING DATE: 1999-11-12
PRIOR PILING DATE: 2000-01-122
PRIOR PILING DATE: 2000-01-124
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PRIOR PILING DATE: 2000-03-23
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  ::: |||::: ||||::298 LeuhrgileAsnLeudspalailePheAsp------GlyLeuThrSerHisGlu 313
   889 CTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTA----AAGAATCTGACATGGCCAAGT 942
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  US-11-097-143-7146; Sequence 7146, Application US/11097143; Sequence 7146, Application US/11097143; Publication No. US20050208558A1; GENERAL INFORMATION: APPLICANT: Venter, J. Craig APPLICANT: et al.
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33.66%
25.44%
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  Percent Similarity:
Best Local Similarity:
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PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR PILING DATE: 2000-02-24
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DB:
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   Alignment Scores:
Pred. No.:
   649
  352
  469
   409
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, NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8943
; LENGTH: 328
  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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   255
   280
  421
  661
                              TYPE: PRT
  Pred. No.:
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  210 ArgAsnAlaGlyProHisAlaSerHisProGlySerGlnGluIleLeuAlaValAlakys 229
   354
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   GGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGAT 531
  8
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   CTGTCTGAGAAAATGCTTGGTAAGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTAC
                              247 ATTGTGGCTACTAAGTGTGGTAGATAT------AAAGAAGGTTTTGATTTCAGT
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   ACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACT
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   592 TACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTT
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  GENERAL INFOGRATION

APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HINGSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATORI
APPLICANTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-08-02
   ; Sequence 8943, Application US/10156761; Publication No. US20030119018A1; GENERAL INFORMATION:
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US-10-156-761-8943
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  412
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70 TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC 129
  130 GAGGCTITICCGICICGGTAICAACTICTICGACACCICCCCGGTATTAIGGAGGAACACIG 189
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99 ThrAlaGlyGlyPheAlaValProAspThrLeuValArgArgProAspTyrSerArgAsp 118
  301 AGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATA 360
  119 GlyValLeuArgSerLeuGluGlySerLeuAsnArgLeuArgLeuAspHisValAspIle 138
  GCTCTTCAGAAACTGAAACAAGAGAGAAAGACCCGGTTCATTGGTATCACTGGTCTTCCG 480
   481 TTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTG 540
   541 TCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCTTACAAG 600
  601 AGCAAAGGIGIGGGIGIGATAAGIGCIICCICATIAGCAAIGGGCCICCIIACAGAACAA 660
   |||
235 HisProAlaAsnAspAlaThrPheAspTyrGlyProAlaSerGluSerAlaLeuArgArg 254
   AGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTG 765
   AlaArgLeuLeuAlaGlyValSerGlyArgHisGlyThrAlaLeuProHisAlaAlaLeu 274
  40
   ::::::|||||| | ||||||
79 IleSerThrLysValdlyArgLeuLeuGluProHisProAlaProThrGlySerAspLeu 98
   20
  ::: ::: ||| |||
195 ValAlaGlyArgTrpThrLeuLeuAspArgThrAlaArgProLeuLeuAspAlaCysAla
   GGTCCTCCT------GAATGGCACCCTGCTTCCCCTGAGCTCTGCA
  ATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCC
   328
101
68
127
46
   Length:
Matches:
Conservative:
Mismatches:
Indels:
   US-10-606-300-12 (1-960) x US-10-156-761-8943 (1-328
; ORGANISM: Streptomyces avermitilis US-10-156-761-8943
   8.53e-32
385.00
49.42%
29.53%
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```
Sequence 23187, Application US/10369493

Sequence 23187, Application US/10369493

Bedication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei

APPLICANT: Slater, Steven C.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION: DIANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION PLANTS WITH IMPROVED PROPERTIES
TITLE OF INVENTION WIMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28

PRIOR PPLICATION NUMBER: US 60/360,039

PRIOR SPELICATION NUMBER: US 60/360,039

PRIOR SEQ ID NOS: 47374

SEQ ID NO 23187
  381
  618
                 ---AspHisAlaGluGlnAlaPheArgGluGlyCysProAlaLeuGluLysLeuArgSer 160
   501
  |||||||
| 61 GluGly------ValValGlyAlaIleGlyAlaGlyMetAsnGlnThrAlaMetLeu 177
  502 CTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTGTCATACTGTCATTACGGCGTT 561
   217
  699
   237
   670 GAATGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCAAAGCCGCAGTTGCTCACTGC 729
   730 AAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAG 789
  258 GluargHisGlyThrThrLeuArgGlyAlaAlaLeuAlaPheCysAlaAlaHisProAla 277
--GATTTCAGTGCTGAGAGAGTAAGAAAGAGTATTGAC 321
   322 GAGAGCTIGGAGAGGCCTTCAGCTTGATTATGTTGACATACTTCATTGCCATGACATTGAG
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   382 TTCGGGTCTCTTGATCAGATTGTGAGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAA
   GAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTT
   619 ATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCT----
  790 ATTTCGTCGGTGTTGGGATGAGCTCTGTCTCACAGGTAGAAGAA 837
   306
100
64
108
12
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Matches:
Conservative:
Mismatches:
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337.50
51.41%
31.35%
20.42%
  ; ORGANISM: Bacillus subtilis
US-10-369-493-23187
   Similarity:
  RESULT 14
US-10-369-493-23187
  Percent Similarity:
Best Local Similarit
   Alignment Scores:
Pred. No.:
  LENGTH: 306
  142
  TYPE: PRT
ORGANISM:
 286
  442
  Query Match:
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  942
   CAGGTAGAAGAAAATGTTGCA---GCAGTTACAGAGCTTGAAAGTCTGGGGATGGATCAA 882
   ||||||| |||:::
----GluAlaTrpLeuAspLeuAspThrAlaAlaThrTrpAlaAla 323
  204
   264
  ----- 285
   GICTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGTCTC 144
   :::||| ||| ::::: ||| || LeuPheThrAlaValHisAlaAlaTrpThrSer 43
   84
  23
   TTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCCTCCGCTCGGAAGT
   GGTAAGGGACTAAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAGTGT
   883 GAAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGT
  328
101
49
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31
   Conservative:
Mismatches:
Indels:
   US-10-606-300-12 (1-960) x US-10-156-761-14813 (1-328)
  Length:
Matches:
   Sequence 14813, Application US/10156761
Sequence 14813, Application US/10156761
Seneral INFORMATION:
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
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APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-30
NUMBER: OF SEQ ID NOS: 15109
SEQ ID NO 14813
  , ORGANISM: Streptomyces avermitilis
US-10-156-761-14813
   GGTAGATATAAAGAA----
   5.09e-30
368.50
50.68%
34.12%
22.29%
  943 GGAATC 948
   324 Gluile 325
   Percent Similarity:
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DB:
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US-10-156-761-14813
  Alignment Scores:
Pred. No.:
   64
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   826
   295
  310
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   TYPE: PRT
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   TyrglnLeuHisgly-----GlyThrIlegluAspAsnIleAspGluThrIleglu 132
  ProAsnValileLysGluTyrValLysLysSer-------AsnIleVal 166
  ::: ::: |||| ||| SerIleMetMetGlnPheSerLeuPheAspArgArgProGluGluTrpLeuProLeuLeu 186
  657
  687
   ::: ||| :::
207 Lyg---ProLeuAspGlnAlaSerGluSerMetLygGlnAsnGlyTyrLeuSerTyrSer 225
   ---CCTGAGCTCAAGTCTGCAAGGCAAAGCC-----GCAGTTGCTCACTGCAAATCAAAG 738
  |||||| :::||| ||||| PheGluGluGluValAlaProAspLeuSer--- 244
   GGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGAGAGTTTCGTCG 798
                                   GGAAGTGTCTTCGGTCCAGTCGCCGAAGATGCCGTCGCCACCGTGCGCGAGGCTTTC 138
   ATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACŢ 258
   AAGTGTGGT---AGATATAAAGAAGGT--------TTTGATTTCAGTGCTGAG 300
  301 AGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGGCTTCAGCTTGATTATGTTGACATA 360
  GTGTTGGTTGGGATGAGCTCTGTCTCACAGTAGAAAAATGTTGCAGCA----- 849
  58
   59 IleValGly------AspAlaIleGlnAsnArgArgHisAspIleIleLeuAlaThr 75
  23
   139 CGTCTCGGTATCAACTTCTTCGACACCTCCCCGGTATTATGGAGGAACACTGTCTGAGAAA
   CCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATA
CGAGCTTTGGGGAACACAGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCCTCCGCTC
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   RESULT 15
US-10-437-963-171001
                                   2
   24
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  199
   259
   76
   96
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Sequence 171001, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICAT: La Rose, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua

```
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plante and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 171001
LENGTH: 945
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  534
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   597 AlaSerAlaAspThrIleArgArgAlaHisAlaValTyrProileThrAlaValGlnMet 716
  535 ATATIGICATACTGICATACGGCGITAAIGATICGACGITGCIGGATITACTACCTTAC 594
  |||| |||| GlufrpSerLeuTrpThrArgAapIleGluGlu-------GluIleIleProLeu 732
   595 TTGAAG-----AGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTC 648
   |||||||
546 LeuGlyThrGlnGlyLeuGluValSerLysLeuGlyPheGlyCysMetGlyLeuThrGly
  CTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAG
  361 CTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGATTGTG-----AGTGAAACA
  :::
TyrTyrGlnHi8ArgIle------AspGlnSerValProlleGluGluThr
  CTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTG
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   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_69273C.1.pep
US-10-437-963-171001
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1107
53
1118
62
  US-10-606-300-12 (1-960) x US-10-437-963-171001 (1-945)
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Matches:
Conservative:
Mismatches:
Indels:
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A
Barbazuk, Brad
   3.52e-26
335.00
47.06%
31.47%
20.27%
  TYPE: PRT
ORGANISM: Oryza sativa
   Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:
   Alignment Scores:
Pred. No.:
   262
  142
   677
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|----------------------------------------------------------------------|----------------------------------------------------------|------------------------------------------|---------------------------------------------------------|-----|----------------------------------------------------------------------|---------------------------------------|-----|---------------------------------------------------------|-------------------------------------------------------------------------------|-------------------------------------------------------|-------------------------------|
| 649 CITACAGAACAAGGICCICCIGAAIGGCACCCIGCITCCCCIGAGCICAAGICIGCAAGC 708 | 753 PheAlaGlyArgAlaAlaValGlnSerIleProSerGluSerTrpLeu 768 | 709 AAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAG | ThrargHisProArgTyrAsnGlyGluAsnLeuGluLysAsnLysValPhe 785 |     | 786 TyrThrargileGluGluLeuAlaThrLysTyrGlyCysSerproAlaGlnLeuAlaLeu 805 | J TCGTCGGTGTTGGTTGGGATGAGCTCTCTCA 825 |     | 826 CAGGTAGAAAATGTTGCAGCAGTTACAGAGCTTGAAAGTCTGGGGATGGAT | ::::::::   :::<br>826 AsnLeuAspAspAspAsnIleGlyAlaValLysValLysLeuSerLysGlu 841 | 886 ACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTG 930 | ii:<br>AlaValProAlaGlyGluGluG |
| 649                                                                  | 753                                                      | 709                                      | 769                                                     | 745 | 786                                                                  | 793                                   | 806 | 826                                                     | 826                                                                           | 886                                                   | 842                           |
| à                                                                    | qq                                                       | ò                                        | ą                                                       | à   | අු                                                                   | È                                     | qq  | 'n                                                      | a                                                                             | à                                                     | qg                            |

Search completed: November 13, 2005, 08:35:31 Job time : 108.5 secs

Scoring table:

Minimum DB Maximum DB

Searched:

Perfect score:

Sequence:

OM nucleic

Run on:

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hypothetical protein T1611.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T04984
B;Bevan, M: Obermaier, B.; Deutschenbaur, S.; Piravandi, B.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, November 1998
A;Reference number: 215393
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A;Residues: 1-319 <BBV>
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A;Cross-references: UNIPROT:O81884; EMBL:ALO31394
A;Experimental source: cultivar Columbia; BAC clone T1611
  aldo-keto reductas
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mocA protein (impo
myo-inositol catab
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   TTTGGTGCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGCCGTCGCC
  1 ATGACGAAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTTAGCGCCGTTGGT
  general
   319
319
0
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0
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A;Introns: 57/2; 133/3; 233/3; 276/3
A;Note: T1611.160
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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  US-10-606-300-12 (1-960) x T04984 (1-319)
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A13183
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E72284
B96632
AI0341
A75289
  AH3033
AH3156
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C64771
  D82644
F95403
  D98252
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  B95902
   1.38e-123
1619.00
100.00%
100.00%
97.94%
  Percent Similarity:
Best Local Similarity:
Query Match:
   16.8
116.7
116.7
116.6
116.6
  Alignment Scores:
305.5
304.5
301.5
301.5
298.5
298.5
  281.83
277.5
276.5
276.5
274.5
274.5
271.5
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   Pred. No.:
   RESULT 1
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-MODEL=frame+ ntp.model -DEV=xlh
-MODEL=frame+ ntp.model -DEV=xlh
-C=Cgn2 1/USPTO spool h/USI0606300/runat 07112005_094819_7311/app_query.fasta_1.1159
-D=Cgn2 1/USPTO spool h/USI0606300/runat_001 -LOOPCE=0 -LOOPEXT=0
-DBT -CPRT=fastan -SUFTX=n2p.rpr -MINMATCH=0.1 -LOOPCE=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UORIGN=200 -THR SCORE=pct -THR MAX=100 -THRNIN=0 -ALIGN=15 -MODE=LOCAL
-OUFFRT=pcc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10606300 @CGN 1 1 27 @runat_07112005_094819_7311 -NCPU=6 -ICPU=3
-NO_WMAP -LARGEQUERY -NGG_SCORES=0 -MAIT -DSPBALOCK=100 -LONGLOG
-DSV_TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
  hypothetical prote
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  November 13, 2005, 08:03:46; Search time 25.5 Seconds (without alignments) 7244.556 Million cell updates/sec
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  hypothetical phypothetical phy
   Description
   atgacgaaaatagagcttcg.....gtggaatccatcagaactaa
   566832
                       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
  - protein search, using frame_plus_n2p model
  Total number of hits satisfying chosen parameters:
   283416 segs, 96216763 residues
  SUMMARIES
  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
  T04984
T28841
GC2405
GS52890
AF2993
H69966
H98303
H99338
H99938
H98303
H969938
   Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
  seq length: 0
seq length: 200000000
   US-10-606-300-12
   В
   Length
   329
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   Copyright
  PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
  BLOSUM62
   Query
  997.9
220.4
221.1.0
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Score

Result

Database :

1619 503 362.5 362.5 346.5 346.5 317.5 317.5 317.5 317.5

246

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465 238 256 573 633

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THAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAG 693
   127 CGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACA 186
   ::::::||||||| ||||||| TyrileSerThrLygValGlyArgPheGluLeuAspTyrAlaArgThrPheAspPheArg 178
   GCTGAGAGAGTAAGAGTATTGACGAGAGCTTGGAGACGCTTCAGCTTGATTATGTT 354
  ATCACTGGTCTTCCGTTAGAT------ATTTTCACTTATGTTCTTGATCGAGTG 513
  ::::: |||||| |||
------AlaProLysLeuTyrPheSerValAsnLeuSerIle 268
  CICAAGICIGCAAGCAAAGCCGCAGIIGCICACIGCAAAICAAAGGGCAAGAAGAICACA 753
  ||||||| ||||||| :::|||:::
|AspSerValGlnGlnValLeuAspAsnLeuGluLeuSerAsnPheSerArgIleThrAsp 359
   .::::: ||||||::::::
  814 AGCTCTGTCTCACAGGTAGAAGAAATGTT--------GCAGCAGTTACAGAG
  514 CCTCCAGGGACTGTCGATGTGTTATTGTCATACTGTCATTACGGCGTTAATGATTCGACG
   187 CTGTCTGAGAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTAC
   247 AITGIGGCTACTAAGIGIGGTAGA-----TATAAAGAAGGITTIGAITTCAGI
  219 TyrGluThrLeuGlnAlaLeuGluMetAlaLysSerSerGlyLysIleArgHisIleGly
  :::||||||
LeuThrGlyTyrProLeuGlyLysLeuValTyrSerPheArgTyrValTrpAsn-----
  GCCTCTCCGCTCGGAAGTGTCTTCGGTCCCAGTCGCCGAAGATGATGCCGTCGCCACCGTG
  GACATA-----CTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGATTGTG---
   406 AGTGAAACAATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGT
   574 ITGCTGGATTTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCA
  AAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGT
   A;Introns: 31/3; 63/3; 101/1; 127/1; 148/3; 204/3; 268/3; 312/3; 371/2
  439
120
120
106
106
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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  7.41e-33
503.00
54.60%
36.81%
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  CESP: F37C12.12
   Score:
Percent Similarity:
Best Local Similarity
Query Match:
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  102
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  320
  63
  121
  295
  179
   355
  634
   694
  257
  269
  Pred. No.:
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T28841
hypothetical protein F37C12.12 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_cevision 29-Oct-1999 #text_change 09-Jul-2004
C;Date: 29-Oct-1999 #sequence_cevision 29-Oct-1999 #text_change 09-Jul-2004
R;Pulton, L.
S;Pulton, L.
S;Pulton, L.
S;Pulton, L.
S;Reference number: Z20530
A;Reference number: Z20530
A;Recession: T28841
A;Resion: T28841
A;Resiones: Jesuparinary; translated from GB/EMBL/DDBJ
A;Residues: 1-439 <FULL>
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   240
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  ArgvalArgLysSerIleAspGluSerLeuGluArgLeuGlnLeuAspTyrValAspIle
  AACAAGGAGATTTCGTCGGTGGTTGGGATGAGCTCTGTCTCACAGGTAGAAGAAAAT
  ValAlaAlaValThrGluLeuGluSerLeuGlyMetAspGlnGluThrLeuSerGluVal
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   GACTACATTGTGGCTACTAAGTGTGGTAGATATAAAGAAGGTTTTGATTTCAGTGCTGAG
  AGAGTAAGAAAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATA
  TTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTGATATTG
  AGCAAAGGTGTGGGTGTAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAA
   GGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCTAGTCTGCAAAGCCGCAGTT
  GCTCACTGCAAATCAAAGGGCAAGAACATCACAAAGTTAGCTCTGCAATACAGTTTAGCA
  GITGCAGCAGITACAGAGCITGAAAGICIGGGGAIGGAICAAGAAACICIGICIGAGGIT
  281
   121
                         41
  181
   61
   241
  81
  301
   101
  361
   121
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   141
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Cidate: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
Cidacession: C83776 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
Cidacession: C83776
Firstamin, H.; Maksone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83776
A;Accession: C83776
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-297 <5370>
A;Cross-references: UNIPROT:Q9X847; GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB047
A;Experimental source: strain C-125
                    549
   591
   216
   651
   236
  969
  256
  697 AAGTCTGCAAGCAAAGCCGCAGTTGCTCCTGCAAATCAAAGGGCAAGAAGATCACAAAG 756
  TrpAspArgLeuValArgIleAlaAlaIleCysArgAsnHisAspValProLeuProAla 276
  816
  873
   315
  GGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTC 138
  23
   oxidoreductase BH1011 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
   185 Leurhrargala------ValargGlualaagpLeuagpLeuileMetValalaGly
  ||||||||
202 ArgTyr-----ThrLeuLeuGluGlnProAlaAlaThrGluValLeuPro
   :::
||||||
237 AlaGinSerGluProLyBArgAspGlyArgTyrGluTyrGlyGlnLeuProAspGluLeu
  490 TICACITAIGIICITGAICGAGIGCCICCAGGGACTGICGAIGIGAIAITGICATACIGI
   592 TACTIGAAGAGCAAAGGIGIGGGIGIGAIAAGIGCIICCICCAITAGCAAIGGGCCICCII
  652 ACAGAACAAGGTCCTCCT------GAATGGCACCCTGCTTCCCCTGAGCTC
   817 TCTGTCTCACAGGTAGAAAATGTTGCA---GCAGTTACAGAGCTTGAAAGTCTGGG
AAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCGTTAGATATT
   550 CATTACGGCGTTAATGATTCGACGTTGCTG-------GATTTACTACCT
  CGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCCTCTCCGCTC
  ::: ||| ||||:::||| |||316 LeuTrpAlaGlu ---LeuAlaGluAlaArgLeuIleProThrPro 329
   874 ATGGATCAAGAAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCT
  297
96
106
31
  A;Gene: BH1011
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
  Length:
Matches:
Conservative:
Mismatches:
Indels:
  US-10-606-300-12 (1-960) x C83776 (1-297)
  1.81e-21
362.50
52.43%
33.33%
21.93%
  Percent Similarity:
Best Local Similarity:
   Alignment Scores:
  79
  13
 330
   C;Genetics:
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Nalternate names: L-fucose dehydrogenase

C;Species: Pseudomonas sp.

C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C;Accession: JC2405, DC250

A;Reference number: JC2405; MJD: 95128037; PMID: 7765723

A;Residues: 1-329 «YMI)

A;Residues: 1-329 «YMI)

A;Residues: 1-329 «YMI)

A;Residues: 1-329 «YMI)

A;Residues: 2-31;147-171;181-195;199-214 «YMZ)

C;Comment: This enzyme is NADPH specific.

C;Superfamily: fission yeast pyridoxine 4-dehydrogenase

C;Keywords: oxidoreductase

E;21-31/Region: NADP binding #status predicted
   429
   AAGAGTATTGACGAGAGCTTGGAGGCTTCAGCTTGATTATGTTGACATACTTCATTGC 369
  82 AGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGCGAGGCTTTCCGT 141
  261
  ----IleMetArgArgTyrLeuAspArg 375
  AladiyargLeuLeuArgProAsnProGluArgArgProSerGlyLeuAspThrAspAsn 104
   |||||||
|LeuGlyAlaPheLeuGlnThr----LysProArgAspGluPheValValSerThrLys 84
   81
   56
   46
  ||||
|AlaAlaAlaAlaAlaGlyLeuAlaIleProAlaLeuGlyTyrGlyAlaAlaABaNvalGly
  CTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAG
 CTTGAAAGTCTGGGGATGGATCAAGAAACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCT
   GCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTTGGTGCCTCTCCGCTCGGA
   ------TATAAAGAAGGTTTTGATTTCAGTGCTGAGAGGTAAGA
   CATGACATTGAGTTCGGGTCTTGATCAGATTGTGAGTGAAACAATTCCTGCTCTTCAG
   329
103
62
122
48
   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                    :::|||
360 ValGluGlnArgValArgAspArg----
   US-10-606-300-12 (1-960) x JC2405 (1-329)
  ::::::|||
376 LeuGluAsnAlaGlyTrp 381
   GTAAAGAATCTGACATGG 936
   9.59e-22
366.00
49.25%
30.75%
  262 TGTGGTAGA-
  Score:
Percent Similarity:
Best Local Similarity:
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Pred. No.
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   22
   7
   27
  202
  67
  82
   271
  145
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   Query Match:
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197 633 217 693 237

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AF2990
oxidoreductase Atu3528 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
   238 AGTGACTACATTGTGGCTACTAAGTGTGGTAGATAT---AAAGAAGGTTTTGATTTCAGT 294
   GCTGAGAGAGAAAAAAAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTT 354
  ::: |||||| |||::
ArgAspPheValArgPheSerValHisArgSerCysGluArgLeuHisThrTyrLeu 118
  GACATACTTCATTGCCATGACATTGAGTTCGGGTCTCTTGATCAGATTGTGAGAACA 414
   ::: ||||::: |||||| :::||| :::||| LeuLysdannagin ::: ||||||||:::||| LeuLysGluLeuArgThrLeuLysdannysGlyVallleLysdannagin 157
  |||:::|||
TyrProlleAspPhelleThrTrpLeuAlaGluTyrCysSerThrGluGluSerAspIle 177
  CTCAAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACA 753
  |||::: ::: |||
LeuArgGluCysAlaSerGlnAlaAlaLysTyrCysGlnGluGlnAsnValAspLeuAla 257
  |||::::::::: |||||||::||||||
AspLeuValTyrLeuHisAspValGluPheValLysPheProAspIleLeu---GluAla
  |||||| :::|||:::::
| AspLeuAlaThrArgTyrAlaIle------SerGluTrpValGlyLys
  -----ATGAGCTCTGTCTCACAGGTAGAAAATGTTGCAGCAGTTACAGAGCTT
   |||| ::: :::::|||
|GulleValLysSerAsnGlyAsnArgLeuSerSerLysAspGlyGlnLeuValGluTyr
   |||||| ::: |||||| ::: ||||| ----SerGluValLeuTyrGlyArgAlaLeuSerAsnLeuArgAsnGluPheProArg
  TTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAG
  GIGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCCGTATTATGGAGGA
   GAAAGTCTGGGGATGGATCAAGAAACTCTGTCTGAGGTTGAAGCT---ATTCTCGAGCCT
   ||| :::::||| ||||| ABDThrTyrPheIleCysThrLysValGlyArgIleGlyAlaGluGluPheAsnTyrSer
  GATTTACTACCTTACTTG-----AAGAGCAAAGGTGTGGTGATAAGTGCTTCTCCA
  ACACTGTCTGAGAAATGCTTGGTAAGGGACTAAAGGCTTTG-----CAAGTCCCTAGA
   GGGACTGTCGATGTTGTCATACTGTCATACGGCGTTAATGATTCGACGTTGCTG
   ATTCCTGCTCTTCAGAAACTGAAACAAGAGGGAAGACCCGGTTCATTGGTATCACTGGT
   -----AATCTGACATGGCCAAGTGGAATC 948
  329
  ::
  CTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCA----
             335
97
57
112
32
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Matches:
Conservative:
Mismatches:
Indels:
  US-10-606-300-12 (1-960) x S52890 (1-335)
   GTAAAG-----
             4.3e-21
358.00
51.68%
32.55%
21.66%
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Best Local Similarity:
Query Match:
DB:
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   66
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  520
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   694
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   292
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Mypothetical protein YMR041c - yeast (Saccharomyces cerevisiae)
MyAlternate names: hypothetical protein YM9532.06c
C;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: $52890,
R;Odell, C: Bowman, S.
Bubmitted to the EMBL Data Library, February 1995
A;Reference number: $52886
A;Reference number: $52880
A;Reference number: $52890
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  TyrilelysGluAlaValLysAspSerLeuArgArgLeuGlnThrAspTyrileAspLeu 115
   TyrGlnLeuHisGly------GlyThrileAspAspProileAspGluThrileGlu 132
   541 TCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTACTACCTTAACG
  601 AGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAA 660
   GGTCCTCTGAA------TGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCAAGC 708
                          CGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTGTCTGAGAAA 198
   28
  75
  ::::::
ProAsnVallleLysGluTyrLeuLysArg------SerAsnIleValSer
  ||| |||||||:: ::::::::||| |||||||:: ||| TyrCysLeualaHisAspvalValAlaThrValAlaAlaAlaGlyAlaSerSerIleAspGln
   481 TTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTATTG
  GluHisGlyValSerValValValArgGlyProValAlaArgGlyLeuLeuSerArgArg
   208 ProteuProgluGlyGluGlyTyrLeuAsnTyrArgTyrAspGluLeuLysLeuLeuArg
  ------AspGluThrLysAlaArgArgIleMetAspGluValLeu
   199 ATGCTTGGTAAGGGACTAAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATTGTGGCTACT
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   GCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATTGGTATCACTGGTCTTCCG
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Cross-references: SGD:S0004644
Map position: 13R
GlyThr--
                          139
  116
   39
   59
   301
   96
  361
   421
   133
  153
  188
   709
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D-three-aldose 1-dehydrogenase (EC 1.1.1.122) [imported] - Agrobacterium tumefaciens (st C;Species: Agrobacterium tumefaciens
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
R;Goodner, B: Hinkle, G:; Gattung, S:; Miller, N.; Blanchard, M.; Qurollo, B:; Goldman, A.; Liu, F:; Wollam, C.; Allinger, M.; Doughty, D:; Scott, C.; Lappas, C.; Markelz, B., Science 294, 2332-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Status: preliminary
  A;Molecule type: DNA
A;Residues: 1-329 <KUR>
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   672
     196 GluIleAspCysIleLeuLeuAlaGlyArgTyr-------ThrLeuLeuAsp 210
  :::::: ||| ||||||::
251 TyrAsnGluAlaValProGluValMetGluArgValCysAlaMetGluAlaHisAlaAla 270
  271 GlyHisGlyValAlaLeuAlaAlaAlaAlaAlaHeenisPheProLeuGlnAsnThrAspVal 290
  :::||||||||||:::|||
291 AlaSerValLeuIleGlyThrAlaLysProAspSerLeuArgArgAsnLeuSerllePhe 310
  70 TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC 129
  130 GAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTG 189
  TCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATT 249
  |||-:::|||
|GlyGlyValPheAsnSerGlyIleLeuAlaThrGlyAlaLysProGlyAlaThrPheAsn
   TGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCAAGCAAAGCCGCAGTTGCTCACTGCAAA
   733 TCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGGAGATT
   793 TCGTCGGTGTTGGGATGAGCTCTGTCTCACAGGTAGAAAATGTTGCA-----
  ----TTACTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGT
  ATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCCCCGTTGGTTTTGGTGCC
   625 GCTTCTCCATTAGCAATGGGCCTCCTTACAGAACAAGGTCCTCCT
  329
102
64
120
10
  Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
  US-10-606-300-12 (1-960) x C98293 (1-329)
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A;Map position: linear chromosome
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  3.69e-20
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48.97%
30.09%
20.96%
   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
  Alignment Scores:
Pred. No.:
  10
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  61
   231
   673
  847
  C:Genetics:
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   C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2990
E;Accession: AF2990
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.B.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell ; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
   ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Reference number: AB2577; MUID:22608550; PMID:11743193

A;Refidues: preliminary

A;Refidues: DNA

A;Residues: 1-329 < KUR>

A;Cross-references: UNIPROT:Q8UA47; GB:AE008689; PIDN:AAL44340.1; PID:g17741932; GSPDB:C

C;Genetics: A;Refidues: Atu3528

A;Map position: linear chromosome
  189
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  |||||||:::|||
|HisAspLeuGluAlaThrThrLeuGlyGluAlaTyrArgHisHisPheGlyIlePhe 158
  AGTGAAACA---ATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATT 462
   523 ACTGTGGATGTGATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGAT 582
  TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC 129
  -----GATTTCAGTGCTGAGAGTAAGA 309
  AAGAGTATTGACGAGAGCTTGGAGGCCTTCAGCTTGATTATGTTGACATACTTCATTGC 369
  GGTATCACTGGTCTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGG 522
  9
  20
  40
  ::::::|||||| |||||||
LeuSerThrLysValGlyArglleLeuLysProAlaGluAlaGlyValThrProAspTyr 98
  69
Species: Agrobacterium tumefaciens
Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
Accession: AF2990
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  ATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCCGTTGGTTTTGGTGCC
  GAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCCGTATTATGGAGGAACACTG
  329
102
120
53
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
  US-10-606-300-12 (1-960) x AF2990 (1-329)
  3.69e-20
346.50
48.97%
30.09%
  Percent Similarity:
Best Local Similarity:
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  Alignment Scores:
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A;Accession: H69966
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-306 < KXDN>
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A;Cross-references: UNIPROT:P54569; GB:Z99116; GB:AL009126; NID:G2634723; PIDN:CAB14294.
A;Experimental source: strain 168
C;Genetics:
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   139 CGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTGTCTGAGAAA 198
  AAGTGTGGT---AGATATAAAGAAGGT------TTTGATTTCAGTGCTGAG 300
  TyrGlnLeuHisGly-----GlyThrIleGluAspAsnIleAspGluThrIleGlu 132
   ::: ::: ||| |||| |||| SerlleMetMetGlnPheSerLeuPheAspArgArgProGluGluTrpLeuProLeuLeu 186
  LysaladiyasnargTrpAspAspdiySerGluGlyTrpTyrTrpAspProSerLysAla 95
  ---CCTGAGCTCAAGTCTGCAAGCAAAGCC-----GCAGTTGCTCACTGCAAATCAAAG
   :::::|||
|IleValGly------AspAlaIleGlnAsnArgArgHisAspIleIleLeuAlaThr
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Lyg---ProLeuAspGlnAlaSerGluSerMetLysGlnAsnGlyTyrLeuSerTyrSer
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   TTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTGCTGGATTTTACTACCTTACTTG
   CCTTACAGAA
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  ::
   AAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCT
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  306
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12
  A,Gene: yqkF
C,Superfamily: fission yeast pyridoxine 4-dehydrogenase
number: A69580; MUID:98044033; PMID:9384377
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Mismatches:
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   conserved hypothetical protein yqkF - Bacillus subtilis
C;Species: Bacillus subtilis
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291 AlaSerValLeuIleGlyThrAlaLy8ProAspSerLeuArgArgAsnLeuSerIlePhe 310
   GlyPheValAspAlaLeuProPheIleValGluTyrAspTyrSerTyrAspGlyIleMet
  310 AAGAGTATTGACGAGAGCTTGGAGAGGCTTCAGCTTGATTATGTTGACATACTTCATTGC
  ---ATTGTG
  ||||||||:::|||
HisAspLeuGluAlaThrThrLeuGlyGluGluAlaTyrArgHisHisPheGlyIlePhe
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||||SlyValPheAsnSerGlyIleLeuAlaThrGlyAlaLysProGlyAlaThrPheAsn
  673 TGGCACCCTGCTTCCCCTGAGCTCAAGTCTGCAAGCCAAAGCCGCAGTTGCTCACTGCAAA
  733 TCAAAGGGCAAGAAGAACAAAGTTAGCTCTGCAATACAGTTTAGCAAACAAGAGATT
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   AGTGAAACA---ATTCCTGCTCTTCAGAAACTGAAACAAGAGGGGAAGACCCGGTTCATT
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  CATGACATTGAGTTCGGGTCTCTTGATCAG----
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  GGTTTT---
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  :::||||||| :::
211 ValLeuThrGlyLysTyrGlnProGlyGluGlnProGlyAlaAspThrArgValGlyArg 230
  705
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  -----LeuAspValLys 299
  886 ACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGT 942
   153 ArgGlyTrpArglleAlaGluIleSerHisLeuAlaAspGlnLeu-----GlyIleAsp
  CTACCTTACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGC
  706 AGCAAAGCCGCAGTTGCTCACTGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTG
   |||||||
|LeuProAlaAlaABnHisTyrGlyLeuGlyValValSerTyrSerProLeuAlaArgGly
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aldo/Keto reductase mocA [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C; Species: Agrobacterium tumefaciens
C; Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
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R; Wood, D.W.; Setubal, J.C.; Kaul, R; Monks, D.; Chen, L.; Wood, G.R.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
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   |||::: ||| ::: ||| ::: |||::: ||||::: ||| ||| 262 ValileThrGlyAlaSerLysIleGlnGlnLeuArgGluAsnIleGlnAlaAlaAsnAla 281
  TCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGATGCCGTCGCCACCGTGCGC 129
  GAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTATTATGGAGGAACACTG 189
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   GTGGCTACTAAG---TGTGGTAGATATAAAGAAGGTTTTGATTTC-----AGTGCT 297
   GAGAGAGTAAGAAAGAGTATTGACGAGAGCTTGAGAGGCTTCACCTTGATTATGTTGAC 357
  69
  :::::: ||| |||||| ::: ||| valAspTyrLeuGlyArgSerAlaLeuLysValSerProLeuSerLeuGlyThr 21
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C;Superfamily: fission yeast pyridoxine 4-dehydrogenase
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Mismatches:
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C;Accession: H90938

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA, Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc. A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Reference number: A99629; MUID:21156231; PMID:11258796

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ProGluSerIleArgGluGluValGluAlaSerLeuGlnArgLeuGlyPheAspTyrIle 130
   AspileTyrMetThrHisTrpGlnSerValProProPheTyrThrProlleAlaGluThr 150
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LeuCysArgAspAsnGlyIleValValGnValTyrSerProLeuGluGlnGlpLyLeuLeu
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   36 GlnIleCysIleAspThrIleLeuGluAlaHisArgCysGlyIleAsnLeuIleAspThr
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-----ProArgGluGlnValValValGluThrLysCysGlyIleValTrpGluArgLys
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   94 GlySerLeuPheAsnLysValGlyAspArgGlnLeuTyrLys------AsnLeuSer
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   hypothetical protein BC82480 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli
C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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   TCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTGCAAGTCCCTAGAAGTGACTACATT 249
   GAGAGAGTAAGAAGAGTATTGACGAGAGCTTGGGCTTCAGCTTGATTATGTTGAC 357
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   GTGGCTACTAAG---TGTGGTAGATATAAAGAAGGTTTTGATTTC-----AGTGCT 297
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LeuAlaThrLysPheValAsnSerHisThrLysGlyProAsnLeuGlyGlyHisSerArg 95
  75
                          ACTCTGTCTGAGGTTGAAGCTATTCTCGAGCCTGTAAAGAATCTGACATGGCCAAGT 942
   GlnLysValAla---AlaHisAlaAlaSerLysGlyValSerAlaAlaAspPheAlaLeu
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   GATGTGATATTGTCATACTGTCATTACGGC---GTTAATGATTCGACGTTGCTGGATTTA
  |||||||
|LeuProAlaAlaAsnHisTyrGlyLeuGlyValValSerTyrSerProLeuAlaArgGly
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   MetMetPheGly-----GlyProThrProAspAspValAlaTyrArgIlelleAsp
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|                                                               | OY 295 GCTGAGAGAGTAAGAAATTGACGAGAGCTTGAGGCTTCAGCTTGATTATGTT 354  Db                                                                       | Db 131 AspileTyrMetThrHisTrpGlnSerValProProPheTyrThrProlleAlaGluThr 150 Qy 415 ATTCCTGCTCTTCAGAAACTGAAACAAGAGGGAAGACCCGGTTCATTGGTATCACTGGT 474 ::: | OY 475 CTTCCGTTAGATATTTCACTTATGTTCTTGATCGAGGGGACTGTCGATGTG 534 | Db 188    GlnAlaLysTyrSeriieLeuABArgAlaMetGluAenGiuLeuLeuFro 205 Qy 592 TACTTGAAGAGCAAAGGTGTGGGTGTGATAAGTGCTTCTCCATTAGCAATGGGCCTCCTT 651 :::                                                                      | Oy 652 ACAGAACAAGGTCCTCCTGAATGGCACCTTCCCCTGAGCTCAGGTAAGCAAA 711                                                                                                                                                                                                                                                                         | Db 243 ValTrpPheGlnArgGluAenMetLeuLysValIleAspMetLeuGluGlnTrpGlnPro 262  Qy 727TGCAAATCAAGGCAAGAAGATCACAAGTTAGCTCTGCAATACAGTTTAGCAAC 783                                                                                                | Qy 784 AAGGAGATTTCGTCGCTGTTCGTTGGATGAGCTCTGTCTCACAGGTAGAAGAAAATGTT 843  187             | QY         844 GCAGCAGTTACAGAGCTTGAAAGTCTGGGGATGGATCAAGAACTCTGTCTG | RESULT 13<br>C64937<br>hypothetical protein b1771 - Escherichia coli (strain K-12)<br>C;Species: Escherichia coli<br>C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004 | C;Accession: C64937 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C. A.; Rose, D.J.; Mau, B.; Shao, Y. Schence 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Title: The A;Geference number: A64720; MUID:97426617; PMID:9278503 | A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Kossuces: 1.326 < |
|---------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------|--------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Qy 652 ACAGAACAAGGTCCTCCTGAATGGCACCCTGCTTCCCCTGAGCTCTGCAAGCAA | Db 243 ValTrpPheGlnArgGluAanMetLeuLyaValIleAapMetLeuGluGlnTrpGlnPro 262  Qy 727TGCAAATCAAAGGCAAGAAGATCACAAAGTTAGCAATACAGTTTAGCAAAC 783  U | Qy     784 AAGGAGATTTCGTCGGTTGGTTGGATGAGTCTCTCACAGGTAGAAAATGTT 843       Db     :::::                                                              | euAsnileAsnieuSerAspAla<br>TC 912<br>  <br>eu 316              | RESULT 12 D85787 hypothetical protein Z2809 [imported] - Escherichia coli (strain O157:H7, substrain EDL9 C;Species: Escherichia coli C;Date: 16.Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 | R. Perras, N.T., 1910. St. Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001 A.Title: Genome sequence of enterohemorrhagic Bscherichia coli 0157:H7. A.Reference number: A85480; MUID:21074935; PMID:11206551 | A;Accessanon: Dss/87<br>A;Status: preliminary<br>A;Residus: 1-236 <sto<br>A;Cross-references: UNIPROT:08XDV3; GB:AE005174; NID:g12515802; PIDN:AAG56760.1; GSPDB:G<br/>A;Experimental source: strain 0157:H7, substrain EDL933</sto<br> | C;Genetics:<br>A;Gene: Z2809<br>C;Superfamily: fission yeast pyridoxine 4-dehydrogenase | 1.61e-17<br>114.00<br>13.44%<br>10.03%<br>19.00%                   | US-10-606-300-12 (1-960) x D85787 (1-326)  Qy                                                                                                                                                       | Oy 61 TTTGGTGCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGAT 111                                                                                                                                                                                                                                                    | 16 TCCCGTATTATGAAGAACACTGTCTGAGAAAATGCTTGGTAAGGGACTAAAGGCTTTG 11:                                                                                                                                                         |

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225
   110
  414
  205
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  591
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   843
   111
   112 -----GCCGTCGCCACCGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACC 165
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   415 ATTCCTGCTCTTCAGAAACTGAAACAAGAGGGAAGACCCGGTTCATTGGTATCACTGGT 474
   171 ValAspAlaAsp------HisIleArgGluTyrLeuGlnTyrGlyGluLeuAspIle 187
   651
   206 LeuCysArgAspAsnGlyIleValValGlnValTyrSerProLeuGluGlnGlyLeuLeu 225
  ---TGCAAATCAAAGGGCAAGAAGATCACAAAGTTAGCTCTGCAATACAGTTTAGCAAAC 783
  9
  17
   35
  55
  |||||||
-----ProkrgGluGlnValValGluThrLysCysGlyIleValTrpGluArgLys 93
   263 LeuCysAlaArgTyrGlnCysThrIleProThrLeuAlaLeuAlaTrpIleLeuLysGln
  ||| :::|||
| LeuGlyThrTrpAlaIleGlyGly-----GlyProAlaTrpAsnGlyAspLeuAspArg
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  94 GlySerLeuPheAsnLysValGlyAspArgGlnLeuTyrLys-----AsnLeuSer
  |||||||
|31 AsplleTyrMetThrHisTrpGlnSerValProProPhePheThrProlleAlaGluThr
   CTTCCGTTAGATATTTTCACTTATGTTCTTGATCGAGTGCCTCCAGGGACTGTCGATGTG
  188 ile-----GlnAlaLysTyrSerIleLeuAspArgAlaMetGluAsnGluLeuLeuPro
  1 ATGACGAAAATAGAGCTTCGAGCTTTGGGGAACACAGGGCTTAAGGTTAGCGCTGGT
   GlnileCysileAspThrileLeuGluAlaHisArgCysGlyileAsnLeuIleAspThr
   -----AGATATAAAGAAGGTTTTGATTTCAGT
  ATATTGTCATACTGTCATTACGGCGTTAATGATTCGACGTTG----CTGGATTTACTACCT
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  243 ValTrpPheGlnArgGluAsnMetLeuLysValIleAspMetLeuGluGlnTrpGlnPro
   61 TTTGGTGCCTCTCCGCTCGGAAGTGTCTTCGGTCCAGTCGCCGAAGATGAT---
           326
103
46
128
66
  226 CAAGTCCCTAGAAGTGACTACATTGTGGCTACTAAGTGTGGT
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Indels:
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Matches:
  US-10-606-300-12 (1-960) x C64937 (1-326)
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30.03%
18.94%
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Best Local Similarity:
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DB:
Alignment Scores:
Pred. No.:
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83427
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Badman, S.; Vuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nuture 406, 999-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc A;Reference number: A82950; MUD:20437337; PMID:10984043
A;Accession: H83427
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95
57
1127
41
  A,Gene: PA1739
C,Superfamily: fission yeast pyridoxine 4-dehydrogenase
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Conservative:
Mismatches:
Indels:
Gaps:
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29.14%
18.48%
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C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Reifle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
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Conservative:
Mismatches:
Indels:
Gaps:
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Pirellula

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1 (bases 1 to 960)

Porro, D. and Sauer.

Ascorbic acid production from yeast

Patent: US 6630330-A 12 07-OCT-2003;

Location/Qualifiers
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Sequence 12 from patent US 6630330.
AR405970.1 GI:40155041
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Antisense suppression of 1-galactose dehydrogenase in Arabidopsis
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Plant J. 30 (5), 541-553 (2002)
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Gatzek, S.
Direct Submission
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Chases I to 960)

S Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J.,
Cheuk, R., Chang, F., Chang, E., Dale, J.M., Goldsmith, A.D.,
Haysshizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M.,
Nguyen, M., Ondera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
Theologis, A. and Ecker, J.R.
Direct Submission
Submitted (14-MAR-2002) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
   Yalouna.

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kin,C.J., Mapers,M.C., Shinn,P., Banh,J. Booser,L., Chan,M.M., Chang,B., Dale,J.M., Dang, J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onders,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Theologis,A., and Ecker,J.R.
   Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
  RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA; RATKEN Arabidopsis Full-Length cDNA); Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

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RS Koesemas B. (Fhen, H.) Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Carninol, P., Dale, J. M., Goldsmith, A. D., Karlin-Neumann, G., Kawal, J., Lam, B., Lee, J. M., Lin, J., Liu, S. X., Miranda, M., Narusaka, M., Nayon, M., Satou, M., Seki, M., Southwick, Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A. Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

Arabidopsis c NA clones

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  S Coesema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, U., Bowser, L., Carrinci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neuman, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Ondera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R. Direct Submission

L. Submitted (06-ANG-2001) Salk Institute Genomic Analysis Laboratory (SIGALL), Plant Biology Laboratory, The Salk Institute for Biology Laboratory, The Salk Institute for Biology Laboratory, The Salk Institute for Biology Laboratory, The Salk Institute for Biology Laboratory Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
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   RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN trabidopsis Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDRAs: Koesema, E., Chen, H., Chenk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J. M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G. Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondera, C.S., Palin, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
  Koesema, E. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

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Direct Submission
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Unpublished
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  AY264803 1221 bp mRNA linear PLN 30-APR-2003
Malus x domestica L-galactose dehydrogenase mRNA, complete cds.
AY264803
  840
  Malus x domestica (cultivated apple)
Malus x domestica
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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1 (bases 1 to 1221)
Beuningl., Bowen,J., Crowhurst,R., Gleave,A., Macrae,E.,
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A Gene Database from Fruit Tree Species
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Unpublished
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AK060431 1234 bp mRNA linear PLN 24-JUL-2003 Oryza sativa (japonica cultivar-group) cDNA clone:001-011-B02, full
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  PLN 24-JUL-2004
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   AB160990 1239 bp mRNA linear PLN 24-JUL-200º
Spinacia oleracea GDH mRNA for L-galactose dehydrogenase, complete
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Caryophyllales; Amaranthaceae; Spinacia.
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   Midda,T., Yabuta,Y., Madhusudhan,R., Motoki,T., Ishikawa,T., Yoshimura,K. and Shigeoka,S.
Direct Submission
Submitted (23-JAM-2004) Yukinori Yabuta, Faculty of Agriculture, Kinki University, Department of Food and Nutrition; 3327-204
Nakamachi, Nara city, Nara 631-8505, Japan
(E-mail;yabuta@nara.kindai.ac.jp, Tel:81-742-43-7273(ex.3416), Fax:81-742-43-2252)
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JOURNAL
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AUTHORS JOURNAL AUTHORS

REPERENCE

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426

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FEATURES

CDS

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Genome Exploration Research Group in Riken: Adachi,J., Alzawa,K., and Genome Science Laboratory in Riken: Adachi,J., Alzawa,K., Akiawa,T., Carninci,P., Fwuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayateu,N., Haramoto,K., Hiramoto,K., Hiramoto,K., Hiramoto,K., Hiramoto,K., Hiramoto,K., Kanagawa,J., Kanagawa,Z., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Osto,N., Saltoh,H., Sakai,C., Sakai,K., Numasaki,R., Ohno,H., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sakai,T., Tagawa,A., Shiraki,T., Tagawa,A., Takahashi,F., Yasunishi,A. and Hayashizaki,Y.
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   The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satch,K., Nagatea,T., Kawagashira,N., Doi,K., Kishhmoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Iida,Y., Sugano,S., Pujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Matsubara,K., Arakawa,T., Fukuda,S., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,M., Imotami,K., Ishii,Y., Itch,M., Xagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
  S Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashizaki, Y., Hayashizamoto, K., Hiraoka, T., Hayashizaki, Y., Hayashizaki, T., Hayashizamoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Ishikawa, R., Imamura, K., Imamura, K., Imamura, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kadawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kushimoto, N., Hiro, J., Myazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Mukamura, M., Namura, M., Obka, B., Ohno, M., Ohtsuki, K., Oka, M., Ooka, M., Oka, M., Ooka, Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinaki, T., Shishiki, T., Sagabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Satuki, Y., Tagami, M., Tagami, Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoko, S., Sano, S.
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NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
   Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Agrobiological Sciences Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-mailskikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
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  FLI_CDNA; oligo-capping.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Trache
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Aramamoco, M. Radan, Sequencing & Analysis Group: Otomo, Y., Iida, Y., Rudman, Y., Rudman, Y., Rusumegi, T., Lu, M., Mana, J., Rodama, T., Rursaaki, T., Kusumegi, T., Lu, M., Mana, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Muzakami, K. Genome Exploration Research Group in Riken: Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Carninoi, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Hiramoto, K., Hiraoka, T., Kadawa, I., Kanagawa, S., Katch, H., Kawai, J., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurthara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakhi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Takaku-Akahira, S., Taqami, M., Taqami, Takeda, Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
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   Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
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   The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kilvchhi.S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kilvchhi.S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikiki, T., Youndai, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shihikii, T., Foundai, T., Foundai, T., Foundai, M., Suzuki, K., Li, C., International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Kroseki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kawai, J., Carninci, P., Adachi, J., Alasawa, K., Rikeni, Kawai, J., Carninci, P., Adachi, J., Masuba, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y., Yoshino, mapping, and annotation of over 28,000 cDNA clones from
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  Yamamoco, M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,

Rujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

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Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K.,

Akimura, T., Arakawa, T., Carninoi, P., Fukuda, S., Hanagaki, T.,

Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Hiramoto, K.,

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Location/Qualifiers
    Yoshino, M. and Hayashizaki, Y. Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice.
   NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kiahimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shiahiki,T. and
Yamamoto,M.
   Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Aubmitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Aurobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:eKkuchi@hias.affrc.go.jp, Tel:al1-29-887-7007), Fax:81-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
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   The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N. Doi, K., Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N. Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, W., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtewiki, K., Shahiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Kucosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nilkura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Casho, N., Ota, Y.,
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Oryza sativa (japonica cultivar-group)
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Embryophyta; Tracheophyta; edons; core eudicots;

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Hoheisel, J., Jesse, T., Heijnen, L., Vos, P., Mewes, H.W., Mayer, K.F.X.
and Schueller, C.
  Submitted (009-NOV-1998) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, B-mail: michael.bevan@bsrc.ac.uk
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Unpublished
   The Arabidopsis sequencing, project.

EU Arabidopsis sequencing, project.

Direct Submission

Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitz 18a, D-82152 Martinaried, FRG, B-mail:

Biochemips biochem.mpg.de, mayer@mips.hiochem.mpg.de Project

Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge

Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
      1 to 65668)
A., van Staveren,M., Dirkse,W., Stiekema,W., Mewes,H.W.,
  E-mail: michael bevandbbsrc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
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  There, T. Chen, H., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J., Bohey, R., Chen, H., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J., Bowser, L., Carninci, P., Chang, B., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Direct Submission
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Plant J. 30 (5), 541-553 (2002)
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Gatzek, S.
Direct Submission
Submitted (23-OCT-2001) Gatzek S., School of Biological Sciences, University of Exeter, Exeter, Ex4 4PS, UNITED KINGDOM
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (Dases 1 to 1092)

2 Koesema,E., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Shinn,P., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Goldanth,A.D., Pham,B.K., Quach,H.L., Sakurai,T., Yandan, Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Palm,C.J., Pham,P.K., Quach,H.L., Sakurai,T., Yamamura,Y., Yu,G., Yu,S., Arabidopsis c NA clones

Unpublished

2 (Dases 1 to 1092)

3 (Dases 1 to 1092)

4 (Dases 2 to 1092)

5 (Dases 3 to 1092)

5 (Dases 3 to 1092)

7 (Dases 3 to 1092)

8 (Sosema,E., Carninci,P., Dale,J.M., Goldanith,A.D., Hayashizaki,Y., Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Jang,P.X., Jones,T., Kamiya,A., Miranda,M., Narusaka,M., Narusak
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   Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
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   The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Meyers, M.C., Shinn, P., Bah, J. Bowser, L., Chan, M.M., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M. Onders, C.S., Palm, C.J., Quech, H.L., Southwick, A., Tang, C.C., Troilumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Davis, R.W.,
  9
Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
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Direct Submission
Submitted (09-NOV-1998) MIPS, at the Max-Planck-Institut fuer
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Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mall: michael.bevane0bbsrc.ac.uk
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  The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Koesema, E., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J. M., Goldenith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Ondera, C.S., Palm, C.J., Pham, P.X., Quach, H.L., Southwick, A., Davis, R.W., Trang, C.C., Toriuni, M., Yamada, K., Yamamura, Y., Yu,G., Yu,S., Davis, R.W., Theologis, A., and Ecker, J.R.
Submitted (06-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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  EIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA; 'RIKEN trabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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   Koesema, E. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as Pis.
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Unpublished
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Arabidopsis thaliana
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| Pred. No.: 2.17e-108 Length: 192861 Score: 1402.50 Matches: 317 Percent Similarity: 53.55\$ Conservative: 0 Best Local Similarity: 53.55\$ Mismatches: 2 Query Match: 86.63\$ Indels: 275 DB: 8 Gaps: 4 US-10-606-300-11 (1-319) x ATCHRIV80 (1-192861)                                                                                                                                                           | Qy         1 MetThrLys1leGluLeuArgAlaLeuGlyAsnThrGlyLeuLysValSerAlaValGly 20 |                                                           | 41 ThrValArgGluAlaPheArgLeuGlylleAsnPhePheAspThrSerPro | Db 4880 ACGTGCGCGAGGCTTTCCGTCTCGGTATCAACTTCTTCGACACCTCCCCGTAAGCACTT 4821  Qy 57 | Db 4820 CTTCTTTTTATATTTTCTAAAGATTACTGATTCTCAATACTGATTCTCTG 4761  Qy 57 | Oy 58                                                                                                                                 | 67                                                                                                                   | Oy 87 LysCysGlyArgTyrLysGluGlyPheAspPheSerAlaGluArgValArgLysSerIle 106                                                                                                                                                                       | Qy 107 AspGluSerLeuGluArgLeuGlnLeuAspTyrValAspIleLeuHisGysHisAspIle 126 | Qy         127 GluPheGlySerLeuAsp | Qy 133                                                                              | Qy 139 IleProAlaLeuGlniysCeulysGlnGluGlyLysThrArgPheileGlyIleThrGly 158        | Qy 159 LeuProLeuAspIlePheThrTyrValLeuAspArgValProProGlyThrValAspVal 178                | Qy 179 IleLeuSerTyrCysHisTyrGlyValAsnAspSerThrLeuLeuAspLeuLeuDroTyr 198            | Qy 199 LeuLysSerLysGlyValGlyValIleSerAlaSerProLeuAlaMetGlyLeuLeuThr 218      | 219  |
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| Rose, M., Hempel<br>Mayer, K.P.X.<br>Unpublished<br>3 (basea<br>Obermaier, B., D<br>and Mayer, K.F.X<br>Unpublished<br>4 (bases 1 to |                                                                                 | annotation and 5 can this frag overlap w                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | / Gene="Ar4g3311<br>/ Gene="Ar4g3313<br>/ Gene="Ar4g3313<br>/ Codon start=1<br>/ Product="hypor<br>/ Protein id="Ca<br>/ Ab xrefe="G1:72<br>/ Ab xrefe="G1:72<br>/ Ab xrefe="UniPr<br>/ LoBs.AllerTVSKLE<br>KSVTRKRESKQVDSL<br>Complement (7525<br>/ Gene="Ar4g3313<br>/ Number=1<br>/ Complement (7591<br>/ Gene="Ar4g3313<br>/ Number=1<br>/ Complement (7667<br>/ Gene="Ar4g3313<br>/ Number=2<br>/ Gene="Ar4g3313<br>/ Number=2<br>/ Gene="Ar4g3313<br>/ Number=2<br>/ Gene="Ar4g3313 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
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| AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL REFERENCE                                                                                  | TOTAL<br>TOURNAL<br>JOURNAL<br>COMMENT                                          | FEATURES SOURCE GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERAL GENERA | CDS exon intron exon intron intron                                                                                                                                                                                                                                                                                                                                                                                                                                                        | exon exon                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| 4041 AAAAGAATGTGATTCTTGTTAACATTTCTGTAGCACTTGTATTGATACACCGTATAAGAG 234                                                                | Db 3921 AGATGCTATACTTCTGAGACTGACATCTTTGTTTCTTAACTCGTACAATCATTGTGATT 3862 Oy 234 | 3801 GTTGGTCTTTGATGAGTATTCAGTAGAAATTAAACAGATTCACATGGACGCTGGTATTT  234                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 238 AlaAlaValAlaHisCysLysSerLysGlyLysLysI<br>3561 GCCGCAGTTCCTCACTGCAAATCAAAGGCAAAGAAGA<br>258 SerLeuAlaAsnLysGluIleSerSerValLeuValC<br>3501 AGTTTAGCAACAGGAGATTTCGTCGGTGTTGGTTC<br>275                                                                                                                                                                                                                                                                                                   | Oy 308 LyskshleuThTrpProSerGlyIleHisGlnAsn 319  Db 3262 AAGAATCTGACATGGCAATCGTCAACACA 3227  RESULT 9  ATCHRIV79/c LOCUS  ATCHRIV79 ATCHRIV79  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  KEYNORDS  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  AL161583.2 G1:7270260  ALCHRIVATOR PETENTIAL ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATTACHED ATT |

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Unpublished

(bases 1 to 1221)

Laing W.A. and Macrae.E.

Direct Submission

Submitted (28-MAR-2003) Gene Technologies Sector, The Horticultural and Food Research Institute of New Zealand, PB 92169, Auckland, New
   PLN 30-APR-2003 complete cds.
  Yauk, Y. K.
   Malus x domestica (cultivated apple)
Malus x domestica
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
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3 1221 bp mRNA linear domestica L-galactose dehydrogenase mRNA,
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40
31
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Matches:
Conservative:
Mismatches:
Indels:
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Laing, W.A. and Macrae, E.
Kiwifruit Leaf Galactose Dehydrogenase
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Yoshimura, K. and Shigeoka, S. Direct Submission Submission Submission Submission Submission Submission Submission Submission Submitted (23-3AN-2004) Yukinori Yabuta, Faculty of Agriculture, Kinki University, Department of Food and Nutrition; 3327-204 Nakamachi, Nara city, Nara 631-8505, Japan (E-mail:yabuta@mara.kindai.ac.jp, Tel:81-742-43-7273(ex.3416), Fax:81-742-43-2252)
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   140
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  160
   AB160990 1239 bp mRNA linear PLN 24-JUL-200º
Spinacia oleracea GDH mRNA for L-galactose dehydrogenase, complete
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AUTHORS
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217

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   Admanco, M. FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Kusumegi, T., Kusumegi, T., Liu, M., Murca, J., Kodama, T., Kursawal, R., Nikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, R. and Murakami, K.
Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninol, P., Fudda, S., Hanagaki, T., Haraoka, T., Arakawa, T., Carninol, P., Fudda, S., Hanagaki, T., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Karoh, H., Kawal, J., Kanagawa, J., Kando, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, H., Sano, H., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Tagami, M., Sano, H., Tagami, Takeda, Y., Tagawa, A., Shiraki, T., Takahashi, F., Takahashi, F., Takahashi, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Takahashi, P., Takahashi, P., Takahashi, P., Takahashi, P., Takahashi, P., Takahashi, P., Tomaru, A., Toya, T., Waki, K., Hayashizaki, Y.
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Direct Submission

Submission

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Agrobiological Sciences, Department of Molecular Genetics, Head of

Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki

305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,

Tel:81-29-838-7007, Pass:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
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  URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagate,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Bhikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
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   The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Magata, T., Kawagashira, N. Doi, K., Kikuchi, S., Satoh, K., Magata, T., Kawagashira, N., Doi, K., Kikuchi, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Kobasshir, Y., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nikura, J., Ikeda, R., Ishibiki, J., Kawanata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RikEshi, Kama, J., Carninci, P., Adachi, J., Alzawa, K., Arakawa, T., Fubuda, S., Kana, A., Hashidume, W., Hayacku, N., Imotani, K., Ishii, Y., Itoh, M., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, Mapping, and annotation of over 28,000 cDNA clones from
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The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchis., Satchk.K., Nagata.T., Kawagashiza,N., Doi,K., Kikuchis.S., Satchk.Y., Nagata.T., Kawagashiza,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Obneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shimiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Pujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Ishibiki,J., Mazuda,H., Kobayashi,M., Xie,O., Lu,M., Narikawa,R., Sugiyama,A., Mazuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawanata,M., Yoshimura,A., Mura,J., Kawai,J., Kawai,J., Kawai,J., Adachi,J., Alzawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayaelu,M., Imotani,K., Ishii,Y., Itoh,M., Salio,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
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  Falls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fulls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fulls Genome States A., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kusomegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Science Laboratory in Riken Genomic Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Haraoka,T., Hashitame,W., Hayatsu,M., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamira,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Konda,X., Kondo,S., Konno,H., Kouda,M.,
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NIAS Rice Pull-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
   Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Submitted (05-DEC-2001) Shoshi Kikuchi, Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
SDS-8602, Japan (E-mail:eKikuchi@milas.affrc.go.jp,
Tel:81-29-838-7007, Fas.81-29-838-7007, This clone is one of the 28K full-length cDNA clones from japonica
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  URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
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Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
Yoshimura, A.
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  64
  84
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